

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:00:35 ; Search time 187 Seconds
(without alignments)
636.747 Million cell updates/sec

Title: US-10-620-562-2

Perfect score: 1426

Sequence: 1 MAPRALPGSAVLAANVFVG.....ETVNGEVPATVVRKRSQTE 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003s.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1426	100.0	271	5	Aae20962 Human TR2
2	1426	100.0	271	7	ADI21099 Novel hum
3	1421	99.6	271	4	AAB88406 Human mem
4	1421	99.6	271	9	ADY63175 Human clo
5	811	56.9	195	4	AAM23972 Human EST
6	811	56.9	195	7	ADI21579 Novel hum
7	477.5	33.5	103	2	AAW88579 Secreted
8	477.5	33.5	103	4	ABBS0346 Human sec
9	477.5	33.5	103	6	ABO44603 Novel hum
10	477.5	33.5	103	7	ABO26083 Human pro
11	332	23.3	181	4	ABBS0685 Human sec
12	332	23.3	181	5	AAE20965 Human TR2
13	332	23.3	181	6	ABO44942 Novel hum
14	332	23.3	181	7	ABO26422 Protein a
15	310	21.7	382	8	ADP29453 Human sec
16	310	21.7	382	8	ADP29451 Human sec
17	307	21.5	408	2	AAV41111 Human TAN
18	307	21.5	430	2	AAV41110 Human TAN
19	307	21.5	430	3	AAV70785 Human tum
20	307	21.5	430	4	AAE05517 Human tum
21	307	21.5	430	4	AAU09901 Human tum
22	307	21.5	430	5	ABG31739 Human TR4
23	307	21.5	430	6	ADA83983 Human TNF
24	307	21.5	430	8	ABO84934 Human can

25	307	21.5	430	8	ABM81290	Abm81290 Tumour-as
26	307	21.5	430	9	ADZ13510	Adz13510 Human can
27	307	21.5	430	9	ADZ13516	Adz13516 Human can
28	307	21.5	457	9	ADZ13508	Adz13508 Human can
29	307	21.5	878	4	AAE02358	Aae02358 Human tum
30	296	20.8	429	7	ADC52548	Adc52548 human tum
31	296	20.8	430	4	AAB95627	Aab95627 Human pro
32	296	20.8	430	5	ABG31740	Abg31740 Human TR4
33	296	20.8	430	6	ABP70909	Abp70909 Human obe
34	295.5	20.7	317	9	ADZ13501	Adz13501 Murine ca
35	295.5	20.7	359	8	ABO84931	AbO84931 Murine ca
36	295.5	20.7	429	9	ADZ13503	Adz13503 Murine ca
37	295.5	20.7	436	4	AAE05518	Aae05518 Mouse tum
38	284	19.9	303	4	AAM93499	Aam93499 Human pro
39	284	19.9	303	8	ADL31172	Adl31172 Human, pol
40	281.5	19.7	245	6	ABR43195	Abr43195 Human REM
41	281	19.7	294	4	AAU87162	Aau87162 Novel Cen
42	281	19.7	294	8	ADI54477	Adi54477 Novel hum
43	278.5	19.5	194	5	AAE20963	Aae20963 Human TR2
44	278	19.5	339	8	ADP29463	Adp29463 Human sec
45	240	16.8	266	8	ADP29422	Adp29422 Human sec

ALIGNMENTS

RESULT 1

AAE20962
ID AAE20962 standard; protein; 271 AA.

XX AAE20962;

DT 01-JUL-2002 (first entry)

XX Human TR21 receptor protein.

KW Human; tumour necrosis factor receptor; TNF; TR21; TR22; immune disorder;
KW autolimmune haemolytic anaemia; rheumatoid arthritis; Addison's disease;
KW allergy; cancer; ulcerative colitis; cardiovascular disorder; epilepsy;
KW myocardial ischaemia; wound healing; neurological disease; infection;
KW cerebral anoxia; gene therapy; immunosuppressive; antiproliferative;
KW cytosstatic; cardiac; vasotropic; neuroprotective; antibacterial;
KW virucide; fungicide; nootropic; ophthalmological.

XX Homo sapiens.

Key	Location/Qualifiers
Peptide	1..29
Region	/label= Signal_peptide
Protein	29..56
Region	/label= Immunogenic_epitope
Protein	30..271
Region	/label= Mature_TR21_protein
Region	81..87
Region	/label= Immunogenic_epitope
Region	109..116
Region	/label= Immunogenic_epitope
Region	142..149
Region	/label= Immunogenic_epitope
Region	168..173
Region	/label= Immunogenic_epitope
Region	192..199
Region	/label= Immunogenic_epitope
Region	204..218
Region	/label= Immunogenic_epitope
Region	233..238
Region	/label= Immunogenic_epitope
Region	262..271
Region	/label= Immunogenic_epitope

WO200207762-A1.

31-JAN-2002.

XX	23-JUL-2001; 2001WO-US023124.	XX	Homo sapiens.
XX	24-JUL-2000; 2000US-0220116P.	XX	WO2003025148-A2.
PR	27-JUL-2000; 2000US-0221143P.	XX	27-MAR-2003.
XX	(HUMA-) HUMAN GENOME SCI INC.	XX	19-SEP-2002; 2002WO-US029964.
XX	Zeng Z, Ruben SM, Rosen CA;	XX	19-SEP-2001; 2001US-0323739P.
XX	WPI; 2002-171948/22.	PR	13-SEP-2002; 2002US-00323739.
DR	N-PSDB; AAD33366.	XX	(HYSB-) HYSBQ INC.
XX	Two novel proteins, TR21 and TR22, which are members of the tumor	XX	Tang YT, Aundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PT	necrosis factor receptor, useful for the diagnosis and treatment of	PI	Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;
PT	immune disorders, cancer, cardiovascular disorders.	PI	Haley-Vicente D;
XX	Claim 11; Fig 1; 248pp; English.	XX	WPI; 2003-354603/33.
XX	The present invention relates to novel human tumour necrosis factor (TNF)	DR	N-PSDB; ADI21815.
CC	receptors, TR21 and TR22 and polynucleotides encoding them. Sequences of	XX	New polynucleotides and secreted proteins, useful for treating myeloid or
CC	the invention are useful in the diagnosis, treatment and prevention of	PT	lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve
CC	cancers (e.g., cancers of the adrenal gland, bone, urogenital or bone	PT	tissue growth or regeneration, in wound healing, and in tissue repair and
CC	marrow, in particular breast and ovarian cancer), immune disorders (e.g.,	PT	replacement.
CC	autoimmune haemolytic anaemia, rheumatoid arthritis, allergies, Addison's	XX	Claim 20; SEQ ID NO 350; 156pp; English.
CC	disease, ulcerative colitis), cardiovascular disorders (e.g., myocardial	XX	The invention relates to an isolated polynucleotide encoding a
CC	ischaeemias), wound healing, neurological diseases (e.g., cerebral anoxia,	CC	polypeptide with biological activity. The polynucleotides and
CC	epilepsy) and infectious diseases such as viral, bacterial, fungal and	CC	polypeptides are useful in diagnostics, forensics, gene mapping,
CC	parasitic infections. They are also useful in gene therapy. The present	CC	identification of mutations responsible for genetic disorders and other
CC	sequence is human TR21 protein	CC	traits, to assess biodiversity, as nutritional sources or supplements.
XX	Sequence 271 AA;	CC	The polynucleotides may also be used as molecular weight markers,
XX	Query Match 100.0%; Score 1426; DB 5; Length 271;	CC	chromosome markers or map related gene positions, or as an antigen to
XX	Best Local Similarity 100.0%; Pred. No. 1.1e-120;	CC	raise anti-DNA antibodies or elicit immune response. The polypeptides are
XX	Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	useful for raising antibodies, as markers for tissues in which the
QY	1 MAPRALPGSAVLAATAAVFVGAVSSPLVAPDNGSSRTLHSRTTTPSPSNDTGNHPEYIA 60	CC	corresponding polypeptide is expressed, for re-engineering damaged or
Db	1 MAPRALPGSAVLAATAAVFVGAVSSPLVAPDNGSSRTLHSRTTTPSPSNDTGNHPEYIA 60	CC	diseased tissues, for treating myeloid or lymphoid cell disorders, in
QY	61 YALVPVFFIMGLFGVLICHLLKKKGYRCTTAEQDIEEEKVEKIELNDSVNENSDTVGQI 120	CC	bone cartilage, tendon, ligament and/or nerve tissue growth or
Db	61 YALVPVFFIMGLFGVLICHLLKKKGYRCTTAEQDIEEEKVEKIELNDSVNENSDTVGQI 120	CC	regeneration, in wound healing, in tissue repair and replacement, in
QY	121 VHYIMKNEANADVLKAMVADNSLYDPESPVTPTGSPPPVSPGLSPGGTGGKHVCCHHL 180	CC	healing of burns, incisions and ulcers, and in treating cancer. The
Db	121 VHYIMKNEANADVLKAMVADNSLYDPESPVTPTGSPPPVSPGLSPGGTGGKHVCCHHL 180	CC	present sequence represents the amino acid sequence of a novel human
QY	181 HTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHKSNOK 240	XX	protein.
Db	181 HTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHKSNOK 240	XX	Sequence 271 AA;
QY	241 ERSLSMSVSGAETVNGEVPAATPVKRRSGTE 271	QY	Query Match 100.0%; Score 1426; DB 7; Length 271;
Db	241 ERSLSMSVSGAETVNGEVPAATPVKRRSGTE 271	XX	Best Local Similarity 100.0%; Pred. No. 1.1e-120;
RESULT 2		XX	Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ADI21099		QY	1 MAPRALPGSAVLAATAAVFVGAVSSPLVAPDNGSSRTLHSRTTTPSPSNDTGNHPEYIA 60
ID	ADI21099 standard; protein; 271 AA.	Db	1 MAPRALPGSAVLAATAAVFVGAVSSPLVAPDNGSSRTLHSRTTTPSPSNDTGNHPEYIA 60
XX	ADI21099;	QY	61 YALVPVFFIMGLFGVLICHLLKKKGYRCTTAEQDIEEEKVEKIELNDSVNENSDTVGQI 120
AC		Db	61 YALVPVFFIMGLFGVLICHLLKKKGYRCTTAEQDIEEEKVEKIELNDSVNENSDTVGQI 120
XX	15-APR-2004 (first entry)	QY	121 VHYIMKNEANADVLKAMVADNSLYDPESPVTPTGSPPPVSPGLSPGGTGGKHVCCHHL 180
DT		Db	121 VHYIMKNEANADVLKAMVADNSLYDPESPVTPTGSPPPVSPGLSPGGTGGKHVCCHHL 180
XX	Novel human protein #74.	QY	181 HTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHKSNOK 240
DE		Db	181 HTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHKSNOK 240
KW	forensic; nutritional source; damaged tissue; diseased tissue;	QY	241 ERSLSMSVSGAETVNGEVPAATPVKRRSGTE 271
KW	myeloid cell disorder; lymphoid cell disorder;	Db	241 ERSLSMSVSGAETVNGEVPAATPVKRRSGTE 271
KW	bone cartilage tissue growth; tendon tissue growth;	RESULT 3	
KW	ligament tissue growth; nerve tissue growth; regeneration; wound healing;		
KW	tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.		

AAB88406
ID AAB88406 standard; protein; 271 AA.
XX AAB88406;
AC
XX
DT 23-MAY-2001 (first entry)
XX
DE Human membrane or secretory protein clone PSEC0162.
XX
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes.
XX
XX Homo sapiens.
XX
XX EPI067182-A2.
XX
XX 10-JAN-2001.
XX
XX 07-JUL-2000; 2000EP-00114090.
XX
XX 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
XX WPI; 2001-093989/11.
XX N-PSDB; AAF93833.
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
XX gene therapy or as candidate target molecules in drug development.
XX
XX Claim 1; SEQ ID NO 180; 609pp + Sequence Listing; English.
XX
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
XX which encode human secretory or membrane proteins represented by AAB88317
XX - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
XX AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
XX invention. The invention also includes methods for the production of
XX antibodies directed against the proteins, and cDNA sequences, which can
XX be used in vaccines. The polynucleotide sequences can be used in gene
XX therapy. The polynucleotide sequences and the proteins they encode may be
XX used in the prevention, treatment and diagnosis of diseases associated
XX with inappropriate secretory protein/membrane protein expression. The
XX nucleic acids and complementary sequences may also be used as DNA probes
XX in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
XX and quantitate the presence of similar nucleic acid sequences in samples.
XX They may also be used to study the expression and function of secretory
XX proteins/membrane polypeptides and their role in metabolism. The
XX polypeptides may be used as antigens in the production of antibodies
XX against them and in assays to identify modulators (agonists and
XX antagonists) of expression and activity. The antibodies and antagonists
XX may also be used as therapeutic agents to down regulate expression and
XX activity. The antibodies may also be used as diagnostic agents for
XX detecting the presence of the polypeptides in samples (e.g. by enzyme
XX linked immunosorbant assay (ELISA). Examples of diseases which may be
XX treated include rheumatoid arthritis and diabetes
XX
XX Sequence 271 AA;
XX
XX Query Match 99.6%; Score 1421; DB 4; Length 271;
XX Best Local Similarity 99.6%; Pred. No. 3.1e-120;
XX Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MAPRALPGSAVLAAAVFVGAVSSPLVAPDNGSSRLHSRTTTPSPSNDTGNHPEYIA 60
XX
XX 1 MAPRALPGSAVLAAAVFVGAVSSPLVAPDNGSSRLHSRTTTPSPSNDTGNHPEYIA 60
XX
XX 61 YALVPVFFIMGLFGLVILCHLLKKKGYRCTTEASQDIEEEKVEKIELNDSVNENSDTVGQI 120
XX
XX 61 YALVPVFFIMGLFGLVILCHLLKKKGYRCTTEASQDIEEEKVEKIELNDSVNENSDTVGQI 120
XX

OY 121 VHYIMKNEANADVLKAMVADNSLYDPESPVTPTSPGPPVSPGPLSPGTPGKHCVCGHHL 180
DB 121 VHYIMKNEANADVLKAMVADNSLYDPESPVTPTSPGPPVSPGPLSPGTPGKHCVCGHHL 180
OY 181 HTVGGVVERDVCHRCRHKRWHPFKPTNKSRESRRPQGEVTVLSVGRPRVTKVBEHKSQK 240
DB 181 HTVGGVVERDVCHRCRHKRWHPFKPTNKSRESRRPQGEVTVLSVGRPRVTKVBEHKSQK 240
OY 241 ERRSLMSVSGAETVNGEVPATPVKRSRGTE 271
DB 241 ERRSLMSVSGAETVNGEVPATPVKRSRGTE 271
RESULT 4
ADY63175
ID ADY63175 standard; protein; 271 AA.
XX
AC ADY63175;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human clone PSEC0162 protein, SEQ ID 180.
XX
KW Gene therapy.
XX
XX Homo sapiens.
XX
XX EPI514933-A1.
XX
XX 16-MAR-2005.
XX
XX 07-JUL-2000; 2004EP-00027228.
XX
XX 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
PR 07-JUL-2000; 2000EP-00114090.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
XX WPI; 2005-203865/22.
XX N-PSDB; ADY63174.
XX
XX Novel isolated polynucleotide encoding human secretory proteins or
XX membrane proteins, useful for examination and diagnosis of abnormality of
XX human secretory proteins.
XX
XX Disclosure; SEQ ID NO 180; 1240pp; English.
XX
XX The present invention relates to novel human secretory proteins or
XX membrane proteins, and their coding sequences. The present sequence is
XX one such protein sequence. The coding sequences of the invention are
XX useful for examination and diagnosis of abnormality of the human
XX secretory proteins and in gene therapy methods. The coding sequences and
XX proteins are useful as candidates for medicines or as target molecules
XX for developing medicines. Antibodies against the proteins of the
XX invention are useful for treating diseases that are associated with the
XX proteins. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained from sequence information
XX supplied by the European Patent Office.
XX
XX Sequence 271 AA;
XX
XX Query Match 99.6%; Score 1421; DB 9; Length 271;
XX Best Local Similarity 99.6%; Pred. No. 3.1e-120;
XX Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MAPRALPGSAVLAAAVFVGAVSSPLVAPDNGSSRLHSRTTTPSPSNDTGNHPEYIA 60
XX
XX 1 MAPRALPGSAVLAAAVFVGAVSSPLVAPDNGSSRLHSRTTTPSPSNDTGNHPEYIA 60
XX
XX 61 YALVPVFFIMGLFGLVILCHLLKKKGYRCTTEASQDIEEEKVEKIELNDSVNENSDTVGQI 120
XX
XX 61 YALVPVFFIMGLFGLVILCHLLKKKGYRCTTEASQDIEEEKVEKIELNDSVNENSDTVGQI 120
XX

PR	06-JUN-1997;	97US-0048964P.
PR	06-JUN-1997;	97US-0048970P.
PR	06-JUN-1997;	97US-0048971P.
PR	06-JUN-1997;	97US-0048972P.
PR	06-JUN-1997;	97US-0048974P.
PR	06-JUN-1997;	97US-0049019P.
PR	06-JUN-1997;	97US-0049020P.
PR	06-JUN-1997;	97US-0049373P.
PR	06-JUN-1997;	97US-0049374P.
PR	06-JUN-1997;	97US-0049375P.
PR	05-SEP-1997;	97US-0057584P.
PR	05-SEP-1997;	97US-0057627P.
PR	05-SEP-1997;	97US-0057628P.
PR	05-SEP-1997;	97US-0057629P.
PR	05-SEP-1997;	97US-0057634P.
PR	05-SEP-1997;	97US-0057635P.
PR	05-SEP-1997;	97US-0057642P.
PR	05-SEP-1997;	97US-0057643P.
PR	05-SEP-1997;	97US-0057644P.
PR	05-SEP-1997;	97US-0057645P.
PR	05-SEP-1997;	97US-0057646P.
PR	05-SEP-1997;	97US-0057647P.
PR	05-SEP-1997;	97US-0057648P.
PR	05-SEP-1997;	97US-0057649P.
PR	05-SEP-1997;	97US-0057650P.
PR	05-SEP-1997;	97US-0057651P.
PR	05-SEP-1997;	97US-0057654P.
PR	05-SEP-1997;	97US-0057661P.
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PR	05-SEP-1997;	97US-0057666P.
PR	05-SEP-1997;	97US-0057667P.
PR	05-SEP-1997;	97US-0057668P.
PR	05-SEP-1997;	97US-0057760P.
PR	05-SEP-1997;	97US-0057761P.
PR	05-SEP-1997;	97US-0057762P.
PR	05-SEP-1997;	97US-0057763P.
PR	05-SEP-1997;	97US-0057764P.
PR	05-SEP-1997;	97US-0057765P.
PR	05-SEP-1997;	97US-0057769P.
PR	05-SEP-1997;	97US-0057770P.
PR	05-SEP-1997;	97US-0057771P.
PR	05-SEP-1997;	97US-0057774P.
PR	05-SEP-1997;	97US-0057775P.
PR	05-SEP-1997;	97US-0057776P.
PR	05-SEP-1997;	97US-0057777P.
PR	05-SEP-1997;	97US-0057788P.
PR	18-DEC-1997;	97US-0070923P.
XX		
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Hu J;	
PI	Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C;	
PI	Florence K, Laflair DW, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR	
PI	Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA;	
PI	Carter KC;	
XX		
DR	WPI: 1999-059865/05.	
DR	N-PSDB: AAV84456.	
XX		
FT	New isolated human genes and the secreted polypeptides they encode -	
FT	useful for diagnosis and treatment of e.g. cancers, neurological	
FT	disorders, immune diseases, inflammation or blood disorders.	
XX		
PS	Claim 11; Page 511; 772pp; English.	
XX		
CC	The invention relates to nucleic acid sequences (AAV84411 to AAV84633)	
CC	encoding human secreted proteins (AAV8534 to AAV88756). The secreted	
CC	protein gene sequences are deposited with the ATCC under deposit numbers	
CC	ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,	
CC	209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host	
CC	cells comprising recombinant vectors containing the nucleic acid	
CC	sequences are used for the recombinant production of the secreted	
CC	proteins. The polynucleotide and amino acid sequences are useful for	

PR 06-JUN-1997; 97US-0048875P.
 PR 06-JUN-1997; 97US-0048876P.
 PR 06-JUN-1997; 97US-0048877P.
 PR 06-JUN-1997; 97US-0048878P.
 PR 06-JUN-1997; 97US-0048879P.
 PR 06-JUN-1997; 97US-0048880P.
 PR 06-JUN-1997; 97US-0048881P.
 PR 06-JUN-1997; 97US-0048882P.
 PR 06-JUN-1997; 97US-0048883P.
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 PR 06-JUN-1997; 97US-0048885P.
 PR 06-JUN-1997; 97US-0048886P.
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 PR 06-JUN-1997; 97US-0048892P.
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 PR 06-JUN-1997; 97US-0048894P.
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 PR 06-JUN-1997; 97US-0049020P.
 PR 06-JUN-1997; 97US-0049373P.
 PR 06-JUN-1997; 97US-0049374P.
 PR 06-JUN-1997; 97US-0049375P.
 PR 05-SEP-1997; 97US-0057584P.
 PR 05-SEP-1997; 97US-0057627P.
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 PR 05-SEP-1997; 97US-0057634P.
 PR 05-SEP-1997; 97US-0057635P.
 PR 05-SEP-1997; 97US-0057642P.
 PR 05-SEP-1997; 97US-0057643P.
 PR 05-SEP-1997; 97US-0057644P.
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 PR 05-SEP-1997; 97US-0057646P.
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 PR 05-SEP-1997; 97US-0057650P.
 PR 05-SEP-1997; 97US-0057651P.
 PR 05-SEP-1997; 97US-0057654P.
 PR 05-SEP-1997; 97US-0057661P.
 PR 05-SEP-1997; 97US-0057662P.
 PR 05-SEP-1997; 97US-0057666P.
 PR 05-SEP-1997; 97US-0057667P.
 PR 05-SEP-1997; 97US-0057668P.
 PR 05-SEP-1997; 97US-0057760P.
 PR 05-SEP-1997; 97US-0057761P.
 PR 05-SEP-1997; 97US-0057762P.
 PR 05-SEP-1997; 97US-0057763P.
 PR 05-SEP-1997; 97US-0057764P.
 PR 05-SEP-1997; 97US-0057765P.
 PR 05-SEP-1997; 97US-0057769P.
 PR 05-SEP-1997; 97US-0057771P.
 PR 05-SEP-1997; 97US-0057774P.
 PR 05-SEP-1997; 97US-0057775P.
 PR 05-SEP-1997; 97US-0057776P.
 PR 05-SEP-1997; 97US-0057777P.
 PR 05-SEP-1997; 97US-0057778P.
 PR 18-DEC-1997; 97US-0070923P.

PR 04-JUN-1998; 98WO-US011422.
 PR 15-JUL-1998; 98US-0092921P.
 PR 30-JUL-1998; 98US-0094657P.
 PR 04-DEC-1998; 98US-00205258.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Hu J;
 PI Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C;
 PI Florence K, Lafleur DW, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR;
 PI Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PU, Endress GA,
 PI Carter KC;
 XX
 DR WPI; 2003-540804/51.
 DR N-PSDB; ACH04740.
 XX
 PT New isolated protein, useful for preparing a composition for diagnosing
 PT or treating cancer, inflammatory, immune or infectious diseases.
 XX
 PS Disclosure; SEQ ID NO 294; 172pp; English.
 XX
 CC The invention relates to an isolated HEMAB80 protein. The protein is
 CC useful for preparing a composition for diagnosing or treating autoimmune
 CC disorders e.g. multiple sclerosis and systemic lupus erythematosus;
 CC haematopoietic cell disorders e.g. agammaglobulinaemia and ataxia
 CC telangiectasia; blood coagulation disorders e.g. afibrinogenemia and
 CC thrombocytopenia; allergy; graft-versus-host disease; inflammatory
 CC conditions e.g. ischaemia-reperfusion injury and arthritis;
 CC hyperproliferative disorders e.g. cancer and purpura; infectious disease
 CC e.g. viral infection and bacterial infection. The polynucleotide or
 CC protein can be used to regenerate damaged tissue e.g. ulcers and
 CC Alzheimer's disease. The present sequence represents the amino acid
 CC sequence of a novel human secreted protein. Note: The sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030065160
 XX
 SQ Sequence 103 AA;
 Query Match 33.5%; Score 477.5; DB 6; Length 103;
 Best Local Similarity 95.0%; Pred. No. 3.3e-35;
 Matches 96; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 Qy 1 MAPRALPGSAVLAARVFGGAVSPVAPDNGSSRTLHSRTTTPSPSNDTGNHPEYIA 60
 Db 1 MAPRALPGSAVLAARVFGGAVSPVAPDNGSSRTLHSRTTTPSPSNDTGNHPEYIA 60
 Qy 61 YALVPVFFINGLFGVLIC-HLLKKGYRCCTEAFQDIEEEK 100
 Db 61 YALVPVFFINGLFGVLIXPKXXKKKGYRCCTEAFQDIEEEK 101
 RESULT 10
 ABO26083
 ID ABO26083 standard; protein; 103 AA.
 XX
 AC ABO26083;
 XX
 DT 10-SEP-2003 (first entry)
 XX
 DE Human protein from novel secreted protein gene 46.
 XX
 KW Human; secreted protein; precerebellin-like protein;
 KW neurodegenerative disorder; behavioural disorder; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; schizophrenia; mania;
 KW dementia; paranoia; psychosis; autism; immune disorder; infection;
 KW inflammation; allergy; liver disorder; hepatoblastoma; jaundice;
 KW hepatitis; immunological disorder; AIDS; leukaemia; rheumatoid arthritis;
 KW sepsis; acne; psoriasis; cancer.
 OS Homo sapiens.
 XX
 PN US6525174-B1.

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XX 25-FEB-2003.
XX 04-DEC-1998; 98US-00205258.
XX 06-JUN-1997; 97US-0048875P.
XX 06-JUN-1997; 97US-0048876P.
XX 06-JUN-1997; 97US-0048877P.
XX 06-JUN-1997; 97US-0048878P.
XX 06-JUN-1997; 97US-0048880P.
XX 06-JUN-1997; 97US-0048881P.
XX 06-JUN-1997; 97US-0048882P.
XX 06-JUN-1997; 97US-0048883P.
XX 06-JUN-1997; 97US-0048884P.
XX 06-JUN-1997; 97US-0048885P.
XX 06-JUN-1997; 97US-0048892P.
XX 06-JUN-1997; 97US-0048893P.
XX 06-JUN-1997; 97US-0048894P.
XX 06-JUN-1997; 97US-0048895P.
XX 06-JUN-1997; 97US-0048896P.
XX 06-JUN-1997; 97US-0048897P.
XX 06-JUN-1997; 97US-0048898P.
XX 06-JUN-1997; 97US-0048899P.
XX 06-JUN-1997; 97US-0048900P.
XX 06-JUN-1997; 97US-0048901P.
XX 06-JUN-1997; 97US-0048915P.
XX 06-JUN-1997; 97US-0048916P.
XX 06-JUN-1997; 97US-0048917P.
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XX 06-JUN-1997; 97US-0048963P.
XX 06-JUN-1997; 97US-0048964P.
XX 06-JUN-1997; 97US-0048970P.
XX 06-JUN-1997; 97US-0048971P.
XX 06-JUN-1997; 97US-0048972P.
XX 06-JUN-1997; 97US-0049019P.
XX 06-JUN-1997; 97US-0049020P.
XX 06-JUN-1997; 97US-0049373P.
XX 06-JUN-1997; 97US-0049374P.
XX 06-JUN-1997; 97US-0049375P.
XX 05-SEP-1997; 97US-0057643P.
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XX 05-SEP-1997; 97US-0057645P.
XX 05-SEP-1997; 97US-0057646P.
XX 05-SEP-1997; 97US-0057647P.
XX 05-SEP-1997; 97US-0057648P.
XX 05-SEP-1997; 97US-0057649P.
XX 05-SEP-1997; 97US-0057650P.
XX 05-SEP-1997; 97US-0057651P.
XX 05-SEP-1997; 97US-0057654P.
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XX 05-SEP-1997; 97US-0057662P.
XX 05-SEP-1997; 97US-0057666P.
XX 05-SEP-1997; 97US-0057667P.
XX 05-SEP-1997; 97US-0057668P.
XX 05-SEP-1997; 97US-0057760P.
XX 05-SEP-1997; 97US-0057761P.
XX 05-SEP-1997; 97US-0057762P.
XX 05-SEP-1997; 97US-0057763P.
XX 05-SEP-1997; 97US-0057764P.
XX 05-SEP-1997; 97US-0057765P.
XX 05-SEP-1997; 97US-0057769P.
XX 05-SEP-1997; 97US-0057770P.
XX 05-SEP-1997; 97US-0057771P.
XX 05-SEP-1997; 97US-0057774P.

05-SEP-1997; 97US-0057775P.
05-SEP-1997; 97US-0057776P.
05-SEP-1997; 97US-0057777P.
05-SEP-1997; 97US-0057778P.
18-DEC-1997; 97US-0070923P.
04-JUN-1998; 98WO-US011422.
15-JUL-1998; 98US-0092921P.
30-JUL-1998; 98US-0094657P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Hu J;
PI Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C;
PI Florence K, Lafleur DW, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR;
PI Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA;
PI Carter KC;
XX WPI; 2003-511926/48.
DR N-PSDB; ACD44550.
XX
XX New precerebellin-like protein, useful for diagnosing or treating
PT neurodegenerative and behavioral disorders, immune disorders, liver
PT disorders, and cancer.
XX
XX Disclosure; SEQ ID NO 294; 156pp; English.
XX
XX The invention relates to an isolated protein comprising amino acid
CC residues 33-205 or 1-205 of a novel human secreted protein appearing as
CC ABO26252. The protein is encoded by one of 238 disclosed cDNA sequences
CC encoding 238 secreted proteins. ABO26252 is a precerebellin-like protein.
CC Also included are a composition comprising the protein and a carrier and
CC an isolated protein produced by expressing the protein cited above by a
CC cell, and recovering the protein. The proteins are useful for diagnosing
CC or treating neurodegenerative and behavioural disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, schizophrenia, mania,
CC dementia, paranoia, psychoses or autism), immune disorders (e.g.
CC infection, inflammation, allergy), liver disorders (e.g. hepatoblastoma,
CC jaundice, hepatitis), immunological disorders (e.g. AIDS, leukaemia,
CC rheumatoid arthritis, sepsis, acne, psoriasis) and cancer. The present
CC sequence is one of the 238 disclosed novel secreted proteins. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at:- seqdata.uspto.gov/sequence.html?DocID=6525174B1
XX
XX SQ Sequence 103 AA;
Query Match 33.5%; Score 477.5; DB 7; Length 103;
Best Local Similarity 95.0%; Pred. No. 3.3e-35;
Matches 96; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 MAPRALPGSAVLAAAVFVGAVSSPLVAPDNGSSRTLHSRTTETTPSPSNDTGNHPEYIA 60
DB 1 MAPRALPGSAVLAAAVFVGAVSSPLVAPDNGSSRTLHSRTTETTPSPSNDTGNHPEYIA 60
QY 61 YALVPVFFIMGLFGLVIC-HLLKKKGVCYRCYTEAEQDIEEEK 100
DB 61 YALVPVFFIMGLFGLVLIXPXXKKKGVCYRCYTEAEQDIEEEK 101
RESULT 11
ABB50685
ID ABB50685 standard; protein; 181 AA.
XX
XX ABB50685;
XX
XX 07-FEB-2002 (first entry)
XX
XX Human secreted protein encoded by gene 46 SEQ ID NO.633.
XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
XX dermatological; immunosuppressive; antiinflammatory; immunostimulant;
XX cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological;
XX neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary;
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Db      76  KKKKVERKXLDNSVNSDITGVQIVHYIMKNEANADVLKAWADNSLYDPESPVTSTPG 135
QY      157  SPPVSPGSLSPGGTTPG 172
Db      136  SPPVSPGLCHQGRGQ 151

RESULT 13
ABO44942
ID  ABO44942 standard; protein; 181 AA.
AC  ABO44942;
XX
DT  02-OCT-2003 (first entry)
DE  Novel human secreted protein #46 fragment #2.
XX
KW  Human; gene therapy; autoimmune disorder; multiple sclerosis; cancer;
KW  systemic lupus erythematosus; haematopoietic cell disorder; allergy;
KW  agammaglobulinaemia; ataxia telangiectasia; blood coagulation disorder;
KW  afibrinogenemia; thrombocytopenia; graft-versus-host disease; arthritis;
KW  inflammatory condition; ischaemia-reperfusion injury; infectious disease;
KW  hyperproliferative disorder; purpura; viral infection; regeneration;
KW  bacterial infection; ulcer; Alzheimer's disease.
XX
OS  Homo sapiens.
XX
XX  US2003065160-A1.
XX
XX  03-APR-2003.
XX
XX  07-DEC-2001; 2001US-00004860.
XX
PR  06-JUN-1997; 97US-0048875P.
PR  06-JUN-1997; 97US-0048876P.
PR  06-JUN-1997; 97US-0048877P.
PR  06-JUN-1997; 97US-0048878P.
PR  06-JUN-1997; 97US-0048880P.
PR  06-JUN-1997; 97US-0048881P.
PR  06-JUN-1997; 97US-0048882P.
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PR  06-JUN-1997; 97US-0048892P.
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PR  06-JUN-1997; 97US-0048896P.
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PR  06-JUN-1997; 97US-0048898P.
PR  06-JUN-1997; 97US-0048899P.
PR  06-JUN-1997; 97US-0048900P.
PR  06-JUN-1997; 97US-0048901P.
PR  06-JUN-1997; 97US-0048915P.
PR  06-JUN-1997; 97US-0048916P.
PR  06-JUN-1997; 97US-0048917P.
PR  06-JUN-1997; 97US-0048949P.
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PR  06-JUN-1997; 97US-0048971P.
PR  06-JUN-1997; 97US-0048972P.
PR  06-JUN-1997; 97US-0048974P.
PR  06-JUN-1997; 97US-0049019P.
PR  06-JUN-1997; 97US-0049020P.
PR  06-JUN-1997; 97US-0049373P.
PR  06-JUN-1997; 97US-0049374P.
PR  06-JUN-1997; 97US-0049375P.
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105-SBP-1997; 97US-0057647P.
105-SBP-1997; 97US-0057648P.
105-SBP-1997; 97US-0057649P.
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105-SBP-1997; 97US-0057651P.
105-SBP-1997; 97US-0057654P.
105-SBP-1997; 97US-0057661P.
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105-SBP-1997; 97US-0057666P.
105-SBP-1997; 97US-0057667P.
105-SBP-1997; 97US-0057668P.
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105-SBP-1997; 97US-0057761P.
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105-SBP-1997; 97US-0057763P.
105-SBP-1997; 97US-0057764P.
105-SBP-1997; 97US-0057765P.
105-SBP-1997; 97US-0057769P.
105-SBP-1997; 97US-0057770P.
105-SBP-1997; 97US-0057771P.
105-SBP-1997; 97US-0057774P.
105-SBP-1997; 97US-0057775P.
105-SBP-1997; 97US-0057776P.
105-SBP-1997; 97US-0057777P.
105-SBP-1997; 97US-0057778P.
105-SBP-1997; 97US-0070923P.
18-DEC-1997; 98WO-US011422.
15-JUL-1998; 98US-0092921P.
30-JUL-1998; 98US-0094657P.
04-DEC-1998; 98US-00205258.

(HUMA-) HUMAN GENOME SCI INC.
Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Hu J;
Olson HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C;
Florence K, Lafleur DM, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR;
Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress CA;
Carter KC;
WPI; 2003-540804/51.
New isolated protein, useful for preparing a composition for diagnosing
or treating cancer, inflammatory, immune or infectious diseases.
Disclosure; Page 28; 172pp; English.
The invention relates to an isolated HEMA80 protein. The protein is
useful for preparing a composition for diagnosing or treating autoimmune
disorders e.g. multiple sclerosis and systemic lupus erythematosus;
haematopoietic cell disorders e.g. agammaglobulinaemia and ataxia
telangiectasia; blood coagulation disorders e.g. afibrinogenemia and
thrombocytopenia; allergy; graft-versus-host disease; inflammatory
conditions e.g. ischaemia-reperfusion injury and arthritis;
hyperproliferative disorders e.g. cancer and purpura; infectious disease
e.g. viral infection and bacterial infection. The polynucleotide or
protein can be used to regenerate damaged tissue e.g. ulcers and
Alzheimer's disease. The present sequence represents the amino acid
sequence of a novel human secreted protein fragment. Note: The sequence
data for this patent did not form part of the printed specification but
was obtained in electronic format directly from USPTO at
seqdata.uspto.gov/sequence.html?DocID=20030085160
Sequence 181 AA;
Query Match 23.3%; Score 332; DB 6; Length 181;
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Best Local Similarity 85.5%; Pred. No. 1.1e-21;
Matches 65; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 97 EEKVEKIELNDNSVNSDVTGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPTPG 156
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Db 76 KKKKVEKKXLDNSVNSDVTGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPTPG 135
QY 157 SPVSPGLSPGGTTPG 172
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Db 136 SPVSPGLCHQGGRQG 151

RESULT 14

ID ABO26422 standard; protein; 181 AA.

AC ABO26422;

DT 10-SEP-2003 (first entry)

Protein associated with novel secreted protein gene 46 #2.

Secreted protein; precerebellin-like protein; sepsis; acne; psoriasis;
neurodegenerative disorder; behavioural disorder; Alzheimer's disease;
Parkinson's disease; Huntington's disease; schizophrenia; mania;
dementia; paranoia; psychosis; autism; immune disorder; infection;
inflammation; allergy; liver disorder; hepatoblastoma; jaundice;
hepatitis; immunological disorder; AIDS; leukaemia; rheumatoid arthritis;
cancer.

Unidentified.

US6525174-B1.

25-FEB-2003.

04-DEC-1998; 98US-00205258.

06-JUN-1997; 97US-0048875P.

06-JUN-1997; 97US-0048876P.

06-JUN-1997; 97US-0048877P.

06-JUN-1997; 97US-0048878P.

06-JUN-1997; 97US-0048880P.

06-JUN-1997; 97US-0048881P.

06-JUN-1997; 97US-0048882P.

06-JUN-1997; 97US-0048883P.

06-JUN-1997; 97US-0048884P.

06-JUN-1997; 97US-0048885P.

06-JUN-1997; 97US-0048892P.

06-JUN-1997; 97US-0048893P.

06-JUN-1997; 97US-0048894P.

06-JUN-1997; 97US-0048895P.

06-JUN-1997; 97US-0048896P.

06-JUN-1997; 97US-0048897P.

06-JUN-1997; 97US-0048898P.

06-JUN-1997; 97US-0048900P.

06-JUN-1997; 97US-0048901P.

06-JUN-1997; 97US-0048915P.

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PR 06-JUN-1997; 97US-0049375P.

PR 05-SEP-1997; 97US-0057584P.

PR 05-SEP-1997; 97US-0057627P.

PR 05-SEP-1997; 97US-0057628P.

PR 05-SEP-1997; 97US-0057629P.

PR 05-SEP-1997; 97US-0057634P.

PR 05-SEP-1997; 97US-0057635P.

PR 05-SEP-1997; 97US-0057642P.

PR 05-SEP-1997; 97US-0057643P.

PR 05-SEP-1997; 97US-0057644P.

PR 05-SEP-1997; 97US-0057645P.

PR 05-SEP-1997; 97US-0057646P.

PR 05-SEP-1997; 97US-0057647P.

PR 05-SEP-1997; 97US-0057648P.

PR 05-SEP-1997; 97US-0057649P.

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PR 05-SEP-1997; 97US-0057666P.

PR 05-SEP-1997; 97US-0057667P.

PR 05-SEP-1997; 97US-0057668P.

PR 05-SEP-1997; 97US-0057760P.

PR 05-SEP-1997; 97US-0057761P.

PR 05-SEP-1997; 97US-0057762P.

PR 05-SEP-1997; 97US-0057763P.

PR 05-SEP-1997; 97US-0057764P.

PR 05-SEP-1997; 97US-0057765P.

PR 05-SEP-1997; 97US-0057769P.

PR 05-SEP-1997; 97US-0057770P.

PR 05-SEP-1997; 97US-0057771P.

PR 05-SEP-1997; 97US-0057774P.

PR 05-SEP-1997; 97US-0057775P.

PR 05-SEP-1997; 97US-0057776P.

PR 05-SEP-1997; 97US-0057777P.

PR 05-SEP-1997; 97US-0057778P.

PR 18-DEC-1997; 97US-0070923P.

PR 04-JUN-1998; 98WO-US011422.

PR 15-JUL-1998; 98US-0092921P.

PR 30-JUL-1998; 98US-0094657P.

XX (HUMA-) HUMAN GENOME SCI INC.

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PI Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon FJ, Endress GA;

PI Carter KC;

XX WPI; 2003-511926/48.

DR New precerebellin-like protein, useful for diagnosing or treating

XX neurodegenerative and behavioral disorders, immune disorders, liver

XX disorders, and cancer.

PS Disclosure; Col 52; 156pp; English.

XX The invention relates to an isolated protein comprising amino acid

CC residues 33-205 or 1-205 of a novel human secreted protein appearing as

CC ABO26252. The protein is encoded by one of 238 disclosed cDNA sequences

CC encoding 238 secreted proteins. ABO26252 is a precerebellin-like protein.

CC Also included are a composition comprising the protein and a carrier and

CC an isolated protein produced by expressing the protein cited above by a

CC cell, and recovering the protein. The proteins are useful for diagnosing

CC or treating neurodegenerative and behavioural disorders (e.g. Alzheimer's

CC disease, Parkinson's disease, Huntington's disease, schizophrenia, mania,

CC dementia, paranoia, psychoses or autism), immune disorders (e.g.

CC infection, inflammation, allergy), liver disorders (e.g. hepatoblastoma,

CC jaundice, hepatitis), immunological disorders (e.g. AIDS, leukaemia,

CC rheumatoid arthritis, sepsis, acne, psoriasis) and cancer. The present

CC sequence is a protein associated with one of the 238 disclosed novel

CC secreted proteins

```
XX SQ Sequence 181 AA;
Query Match 23.3%; Score 332; DB 7; Length 181;
Best Local Similarity 85.5%; Pred. No. 1.1e-21;
Matches 65; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 97 EEEKVKIELNDSVNSDVGQIVHYIMKNEANADVLKAWADNSLYDPSPVTPSTPG 156
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Db 76 KKKKVEKXLDNSVNSDVGQIVHYIMKNEANADVLKAWADNSLYDPSPVTPSTPG 135

QY 157 SPVSPGCLSPGGTTPG 172
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Db 136 SPVSPGCLHQGGGQQ 151

RESULT 15
ADP29453
ID ADP29453 standard; protein; 382 AA.
XX AC ADP29453;
XX DT 12-AUG-2004 (first entry)
XX DE Human secreted protein SEQ ID #220.
XX KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX OS Homo sapiens.
XX PN WO2004035732-A2.
XX PD 29-APR-2004.
XX PF 28-AUG-2003; 2003WO-US026780.
XX PR 29-AUG-2002; 2002US-0406576P.
PR 29-AUG-2002; 2002US-0406579P.
PR 29-AUG-2002; 2002US-0406585P.
PR 29-AUG-2002; 2002US-0406588P.
PR 29-AUG-2002; 2002US-0406608P.
PR 29-AUG-2002; 2002US-0406611P.
PR 29-AUG-2002; 2002US-0406612P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406640P.
PR 29-AUG-2002; 2002US-0406642P.
PR 29-AUG-2002; 2002US-0406646P.
PR 29-AUG-2002; 2002US-0406653P.
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PR 29-AUG-2002; 2002US-0406666P.
PR 17-SEP-2002; 2002US-0410946P.
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PR 17-SEP-2002; 2002US-0410948P.
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PR 17-SEP-2002; 2002US-0410953P.
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PR 17-SEP-2002; 2002US-0411041P.
PR 17-SEP-2002; 2002US-0411045P.
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PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411101P.
PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
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PR 02-MAY-2003; 2003US-0467203P.
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PR 19-MAY-2003; 2003US-0471306P.
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PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
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PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX XX
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX XX
PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX XX
DR WPI; 2004-348438/32.
XX XX
PT New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX XX
PS Claim 1; SEQ ID NO 1451; 428pp; English.
XX XX
CC The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPONEB and is not in the specification.
XX XX
SQ Sequence 382 AA;

Query Match 21.7%; Score 310; DB 8; Length 382;
Best Local Similarity 32.1%; Pred. No. 2.8e-19;
Matches 84; Conservative 36; Mismatches 72; Indels 70; Gaps 12;

QY 44 TPSPSNDTGNCHPE-----YIAYALVPVFFINCLFGVLCHLLKKYGRCTTAE----- 93
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 102 TRQPGNGTRAGGPEETAQYAVIAIVPFCMLGLLGLVCLNLLKRRGYHCTAHEVGP 161
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 94 ----QDIEEKVEKIELNDSVNSDVGQIVHYIMKNEANADVLKAWADNSLYDPSP 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 162 GGGGSGTSD-----ANEDTIGVLVPLITEKENAALBELKE---YHSKQL 205
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 150 VTPSTPGSPVSPGSLSPGGTPEKRVKVC--GHHLHTVGGV--VERDVCRCRHRWHFI-- 203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 206 VQTS---HRPVSKLPAPPNPV--HICPHRHLLHTVQGLASLSPGCCSRCSQKKWPEVLL 260
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Qy	204	-----KPTNKSRE-SRPRQGEVTVLSVGRFRVTKVYHKSNOKERRSLM	246
Db	261	SPEAVAATTPVPSLLPNPTRVPKAGAKAGQGEITILSVGRFRVARI-----PEQRTSS	314
Qy	247	SVSGAETVN-----GEVPATP	262
Db	315	MVSEVKTITEAGPSWGDLPDSP	336

Search completed: February 23, 2006, 12:03:53
Job time : 190 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:09:38 ; Search time 18 Seconds
(without alignments)
224.136 Million cell updates/sec

Title: US-10-620-562-2

Perfect score: 1426

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications_AA_New.*
- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PUB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PUB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PUB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	307	21.5	430	7	US-11-042-814-2
2	295.5	20.7	436	7	US-11-042-814-4
3	97.5	6.8	447	7	US-11-072-512-2688
4	97	6.8	287	7	US-11-198-819-6
5	97	6.8	287	7	US-11-198-819-8
6	87.5	6.1	948	6	US-10-485-517-131
7	85.5	6.0	367	6	US-10-888-962-6
8	85	6.0	241	7	US-11-072-512-2203
9	85	6.0	377	7	US-11-240-769-67
10	84.5	5.9	954	6	US-10-467-962B-31
11	84	5.9	1344	7	US-11-072-512-2452
12	82.5	5.8	399	6	US-10-467-657-1672
13	82.5	5.8	1140	7	US-11-169-232-104
14	82.5	5.8	1363	7	US-11-169-232-52
15	82.5	5.8	1404	7	US-11-169-232-2
16	82.5	5.8	1404	7	US-11-169-232-62
17	82	5.8	948	6	US-10-523-477-14
18	81.5	5.7	626	7	US-11-072-512-2827
19	81	5.7	220	7	US-11-169-232-96
20	80.5	5.6	714	7	US-11-124-367A-268
21	79.5	5.6	254	6	US-10-714-887-126
22	79.5	5.6	427	6	US-10-714-887-122
23	79.5	5.6	619	7	US-11-052-554A-229
24	79.5	5.6	2910	7	US-11-087-100-2
25	79.5	5.6	2910	7	US-11-087-084-2

Sequence 2, Appli
Sequence 522, App
Sequence 4486, Ap
Sequence 374, App
Sequence 31, Appl
Sequence 444, App
Sequence 442, App
Sequence 445, App
Sequence 443, App
Sequence 441, App
Sequence 446, App
Sequence 79, Appl
Sequence 5, Appli
Sequence 762, App
Sequence 70, Appl
Sequence 983, App
Sequence 981, App
Sequence 982, App
Sequence 3, Appli
Sequence 51, Appl

26 79.5 5.6 2910 7 US-11-087-085-2
27 78.5 5.5 294 6 US-10-485-788A-522
28 78.5 5.5 831 6 US-10-467-657-4486
29 78 5.5 619 7 US-10-485-517-374
30 78 5.5 2161 7 US-11-126-313-31
31 78 5.5 2760 7 US-11-124-367A-444
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35 78 5.5 3027 7 US-11-124-367A-441
36 77 5.4 1972 7 US-11-124-367A-446
37 76.5 5.4 431 7 US-11-058-735-79
38 76.5 5.4 441 7 US-11-175-153-5
39 76 5.3 227 7 US-11-176-830-762
40 75.5 5.3 296 7 US-11-169-232-70
41 75.5 5.3 828 6 US-10-995-561-983
42 75.5 5.3 918 6 US-10-995-561-981
43 75.5 5.3 1019 6 US-10-995-561-982
44 75.5 5.3 1463 6 US-10-971-982-3
45 75 5.3 274 6 US-10-353-783-51

ALIGNMENTS

RESULT 1

US-11-042-814-2
; Sequence 2, Application US/11042814
; Publication No. US20060024267A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; APPLICANT: Welch, Andrew A
; APPLICANT: Boedigheimer, Michael J
; APPLICANT: Shu, Junyan
; APPLICANT: Gary M. Fox
; TITLE OF INVENTION: TNF/OPG-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/36854
; CURRENT APPLICATION NUMBER: US/11/042,814
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: US/10/146,574
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/724,037
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-042-814-2

Query Match 21.5%; Score 307; DB 7; Length 430;
Best Local Similarity 31.0%; Pred. No. 5.7e-21;
Matches 84; Conservative 36; Mismatches 69; Indels 82; Gaps 12;

QY 44 TPSPSNDTGNHGPE-----YIAVALVPFIMGLFGLVILCHLLKKKGYRCTTAE----- 93
144 TRQFGNGTRAGGEEETAAQYAVIAIVPFCMLGILVNCNLLKRYKGYHCTAKVEVGP 203
QY 94 -----ODIEEKVEKIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVAD 140
204 GGGGGGINPAYRTD-----ANEDTIGVLVRLITEKENNAALEELKE 247
QY 141 NSLYDPESPVPPTGSPSPVSPGLSPGTPGKHC--GHLHTVGV--VERDVCHRCR 196
248 ---YHSKQLVQTS---HRPVSKLPAPPNPV--HICPHRHLLHTVQGLASLGPCCSRCS 299
QY 197 HKQWHFI-----KPTNKSRE--SRPRQGEVTVLSVGRFRTVKVEHS 237
300 QKKWPEVLLSPEAVATTVPVSLLPMPTRVPKAKAGROGBITILSVGRFVRARI----- 355
QY 238 NOKERSLSMSGAEVTN-----GEVPATP 262

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Db 356 --PEQRTSSMVSEVKTTITEAGPSWGLPDSP 384

RESULT 2
US-11-042-814-4
; Sequence 4, Application US/11042814
; Publication No. US20060024267A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; APPLICANT: Weicher, Andrew A
; APPLICANT: Boedighelmer, Michael J
; APPLICANT: Shu, Junyan
; APPLICANT: Gary M. Fox
; TITLE OF INVENTION: TNF/OPG-LIKE MOLECULES AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/11/042,814
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: US/10/146,574
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/724,037
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-042-814-4

Query Match 20.7%; Score 295.5; DB 7; Length 436;
Best Local Similarity 30.6%; Pred. No. 6.8e-20;
Matches 82; Conservative 36; Mismatches 89; Indels 61; Gaps 12;

QY 31 NGSRTLHSTETTPSPSNDTGNHPE-----YIAYALVPVFFIMGLFGVLIHLLKKKG 85
Db 148 NGEPR-----QPGNGTRAGGPEETAQAQAVIAIVPVCLMGLLGLVLCNLLKKG 197

QY 86 YRCTTEAQDIEE-----EKVEKIELNDSVNENSDTWCQIVHYIMKNEANA-----DVLKAM 137
Db 198 YHCTAQKEVGPSPGGGGGINPAYRTEDANE--DTIGVLVRLITEKKENAAALELLKEY 255

QY 138 VADNSLYDPESPVTPTSPGPPVSPGSLPGGTPGKHVC--GHHLHTVGGV--VERDVC 193
Db 256 HSKQLVQTSRFPVRLLPSPSI-----PHICPHHLLHTVQGLASLGPCCS 303

QY 194 RCHKRWHTF-----KPT---NKSR-----ESRPRQGEVTVLSVGRFRVTKVE 234
Db 304 RCSQK-WPEVLLSPAAAAATTPATLLPTASRAPKASAKPGRQGEITILSVGRFRVARIP 362

QY 235 HKSQKERSLSMSVSGAETVNGEVPATP 262
Db 363 EQRTSLLSEVKTTITEAGPSWGLPDSP 390

RESULT 3
US-11-072-512-2698
; Sequence 2698, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGIYAMA, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAWATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO

; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2688
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2688

Query Match 6.8%; Score 97.5; DB 7; Length 447;
Best Local Similarity 20.6%; Pred. No. 0.18;
Matches 72; Conservative 37; Mismatches 87; Indels 153; Gaps 16;

QY 29 PDNGSSRTLH-----SRTETTPSNDTGNHPEYI 59
Db 73 PDNTSKTTDCLQTKGFSNSTEHRGSAQVQKQVGFNNCLNRGQSSFORSYSSSHSPAKI 132

QY 60 AYALVPVFFIMGLFGVLIHLLKKGYRCTTEAQDIEEKVEKIELNDSVNENSDTV-G 118
Db 133 -----QRATQEPVAKIEGTQESQMVGSSSTREKASTVLS 166

QY 119 QIVHYIMKNEA-----NADVLKAM-----VADNSLY----- 144
Db 167 QIVASIQPPQSPETPQSGPKACSVBELYAIPPDADVAKSTPKSTVPRKSLFTSPSGE 226

QY 145 -----DPB-SPVTPS-----TPGSPVPSVPGSLPGGTPGKHVCVGHLLH 181
Db 227 AEAPQTTDPTTKVQKDPISIKVPVTPSPSKLVTSPQSEPPAPFF-PPRSTSSPHAGNLLQ 285

QY 182 TVGGVVERDVCHRCRH-KRWHTFKPTNKSR-----ESRPRQGEVTVL 223
Db 286 -----RHFTNW--TKPTSPTRSTAESVHLHSEGSRAADAKPKW--ISFK 327

QY 224 SVGRFRVTKVE-HKSQKERRSLMSVSGAETVNGEVPATPVKERSGTE 271
Db 328 SFFRRKTDDEDDKEKERKGLVGLDG--TVIHMLPPPPVQRHHWFE 374

RESULT 4
US-11-198-819-6
; Sequence 6, Application US/11198819
; Publication No. US20050287582A1
; GENERAL INFORMATION:
; APPLICANT: Adema, Goease Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/198,819
; FILING DATE: 04-AUG-2005
; CLASSIFICATION:
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NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, V1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/11/198.819

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; EDUCATION NO.: US24005052362359AL
;
; GENERAL INFORMATION:
;
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
;
; TITLE OF INVENTION: Antigenic Polypeptides
;
; FILE REFERENCE: P100629W0
;
; CURRENT APPLICATION NUMBER: US/10/485,517
;
; CURRENT FILING DATE: 2004-02-02
;
; PRIOR APPLICATION NUMBER: GB 0118825.9
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; PRIOR FILING DATE: 2001-08-02
;
; PRIOR APPLICATION NUMBER: GB 0200349.9
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; PRIOR FILING DATE: 2002-01-09
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; NUMBER OF SEQ ID NOS: 424
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; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 131

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; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-131

Query Match      6.1%; Score 87.5; DB 6; Length 948;
Best Local Similarity 21.2%; Pred. No. 4.4;
Matches 55; Conservative 30; Mismatches 94; Indels 81; Gaps 12;

QY 26 LVAPDNGSSRTLSRSTRTTTPSPNDTNGHPEY-----IAYALVPVFFIMGLFGVLI 77
Db 714 IVDFDSDVPQIHQNGNGSFFEDTEKPKVEQGGNIIDIDFDSVP-----761
QY 78 CHLLKKKGYRCTTE-ABQDIEEKVE-KIELNSVNSNSDVGQIV-HYIMKNEANADVL 134
Db 762 -HI---HGFNKHTEIIEEDTNKQPNYQFGHNSVDFEEDTLFQVSGHNEGQQTIEDTT 817
QY 135 KAMVADNSLYDPSPVTPSTFGSP-----PVSPGPLSP--GGTPGKHVCGHH 179
Db 818 PPVV-----PTPTTPEVPSRPETPTPTPEVPSRPETPTPTPEVPTGPKP-----865
QY 180 LHTVGGVVERDVCHRCRKHWHFIKPTNK--SRESRRRQGEVT--VLSVGRFRVTKVEH 235
Db 866 -----IPPAKEBPKKPSKEVQGGKVVTVPVIEINEKVKAVVPT 902
QY 236 KSNOKERRSLMSVSGAETVN 255
Db 903 KKAQSKKSELPTGGEESTN 922

RESULT 7
US-10-888-962-6
; Sequence 6, Application US/10888962
; Publication No. US20050266531A1
; GENERAL INFORMATION:
; APPLICANT: Saint Louis University
; APPLICANT: Ray, Ranjit
; APPLICANT: Yie-Hwa, Chang
; APPLICANT: Ray, Ratna
; APPLICANT: Basu, Arnab
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
; TITLE OF INVENTION: Growth
; FILE REFERENCE: SLU 03-013 PCT
; CURRENT APPLICATION NUMBER: US/10/888,962
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/487,126
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-888-962-6

Query Match      6.0%; Score 85.5; DB 6; Length 367;
Best Local Similarity 25.8%; Pred. No. 1.8;
Matches 58; Conservative 23; Mismatches 93; Indels 53; Gaps 13;

QY 25 PLVAPDNGSSRTLSRSTRTTTP--SPNDTNGHPEYIAYA-LVPV-----FFIMGLFG 74
Db 150 PLLAPLN-DTRVVHAAKAALAAFAAQNNGSNFQLEISRAQLVLPSTVFTVSGTDC 208
QY 75 V-----LCHLLKKKGYR-CTTEAQDIEEKVEKIELNSVNSNSDVGQIVHYIMK 126
Db 209 VAKEATEAAKCNLLAEKQYGFCKATLSEKLGAEV---AVTCTVFQTPVTSQ---POP 261
QY 127 NEANADVLKAMVADNSLYDPSPVTPSTFGSPVSPGPLSPGCT-PGKHVC-----GHHL 180
Db 262 EGANEAV-----PTPVVDPAPEPPLGAPGLPPAGSPDPSHVLAAAPGHQL 309
QY 181 HTVGGVVERDVCHRCRKHWHFIKPTNKRE--SRPRRQGEVTVLSVG 226
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-131

Query Match      6.1%; Score 87.5; DB 6; Length 948;
Best Local Similarity 21.2%; Pred. No. 4.4;
Matches 55; Conservative 30; Mismatches 94; Indels 81; Gaps 12;

QY 26 LVAPDNGSSRTLSRSTRTTTPSPNDTNGHPEY-----IAYALVPVFFIMGLFGVLI 77
Db 714 IVDFDSDVPQIHQNGNGSFFEDTEKPKVEQGGNIIDIDFDSVP-----761
QY 78 CHLLKKKGYRCTTE-ABQDIEEKVE-KIELNSVNSNSDVGQIV-HYIMKNEANADVL 134
Db 762 -HI---HGFNKHTEIIEEDTNKQPNYQFGHNSVDFEEDTLFQVSGHNEGQQTIEDTT 817
QY 135 KAMVADNSLYDPSPVTPSTFGSP-----PVSPGPLSP--GGTPGKHVCGHH 179
Db 818 PPVV-----PTPTTPEVPSRPETPTPTPEVPSRPETPTPTPEVPTGPKP-----865
QY 180 LHTVGGVVERDVCHRCRKHWHFIKPTNK--SRESRRRQGEVT--VLSVGRFRVTKVEH 235
Db 866 -----IPPAKEBPKKPSKEVQGGKVVTVPVIEINEKVKAVVPT 902
QY 236 KSNOKERRSLMSVSGAETVN 255
Db 903 KKAQSKKSELPTGGEESTN 922

RESULT 8
US-11-072-512-2203
; Sequence 2203, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAL, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: TRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2203
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2203

Query Match      6.0%; Score 85; DB 7; Length 241;
Best Local Similarity 20.8%; Pred. No. 1.1;
Matches 40; Conservative 38; Mismatches 76; Indels 40; Gaps 9;

QY 53 NGHPEYIAYALVPVFFIMGLFGLVLIHLLKKGYRCTTEAQDIEE-----EKV-----101
Db 4 NDAKEYLARREIPQLF-ESLLNGLMC-----SKPEDPVEYLESCLQVKELGGC 51
QY 102 EKIELNSVNSNSDVT-----GQIVHYIMKNEANADVLKA--MVADNSLYDPSPVTPST 154
Db 52 DKVKWDTFVSQEKKTLPPLNGGQSRSLRNESDLDSETAELIESEVFPDTRP-----R 107
QY 155 PGSPVSPGPLSPGCTPGKHVC---CHHLHTVGGVVERDVCHRCRKHWHFIKPTNKRE 211
Db 108 PKILLVIGPGSGKQSLKIAERYQYISVIGELLRKIKHSTSNRKWSLIAKIITTE 167
QY 212 SRPRRQGEVTVLSV 225
Db 168 LAPQ---ETITTEI 178

RESULT 9
US-11-240-769-67
; Sequence 67, Application US/11240769
; Publication No. US20060036089A1
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: 33 Human Secreted Proteins
; FILE REFERENCE: P2037P1C2
; CURRENT APPLICATION NUMBER: US/11/240,769
; CURRENT FILING DATE: 2005-10-03
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;; PRIOR APPLICATION NUMBER: 09/997,131
;; PRIOR FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: 09/628,508
;; PRIOR FILING DATE: 2000-07-28
;; PRIOR APPLICATION NUMBER: PCT/US00/03062
;; PRIOR FILING DATE: 2000-02-08
;; PRIOR APPLICATION NUMBER: 60/119,468
;; PRIOR FILING DATE: 1999-02-10
;; NUMBER OF SEQ ID NOS: 173
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 67
;; LENGTH: 377
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (164)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (213)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-11-240-769-67

Query Match 6.0%; Score 85; DB 7; Length 377;
Best Local Similarity 22.6%; Pred. No. 2.1;
Matches 53; Conservative 28; Mismatches 66; Indels 88; Gaps 14;

Qy 59 IAAVALVPVFFIMGLFGLVILCHLKKGYRCRTTEAEQDIEBEKVKIELNDSVNSDTVG 118
Db 183 IINSVVVFFLGSGLSIIITLRK-----DIANYKED-DIEDTMEESG---W 227
Qy 119 QIVHYIMKNEANADVLKAMVADNSLYDPSTPTGSPVSPGSLSPGG-----T 170
Db 228 KLVH-----GDVFR-----PPVPHDPQLAGLRHSVLYD 258
Qy 171 PGKHVCGH-----HLHT-----VGVVVERDVCHCRHKRW-----HFKTPNKS 209
Db 259 PHRHLCSHAWDAVALPGSGSHDLSLLPLHVHGGVWRIFC-----WPSVPHPKRP---S 308
Qy 210 RESRPRQGEVTVLSVGRFRTVKE--HKSNOKERRSLMSVSGAETYN--GEVPA 260
Db 309 VEBSLLYGN-SVPWCGFWHLRLIELHLGKALIRSGALSHHGGSAVHVVRDLPA 362

RESULT 10
US-10-467-962B-31
;; Sequence 31, Application US/10467962B
;; Publication No. US20050246784A1
;; GENERAL INFORMATION:
;; APPLICANT: Plesch, Gunnar
;; APPLICANT: Blau, Astrid
;; APPLICANT: Daeschner, Klaus
;; APPLICANT: Klein, Mathieu
;; TITLE OF INVENTION: Identification of Herbicidally Active Substances
;; FILE REFERENCE: 2000.857
;; CURRENT FILING DATE: 2003-08-14
;; PRIOR APPLICATION NUMBER: US/10/467,962B
;; PRIOR FILING DATE: 2002-02-13
;; NUMBER OF SEQ ID NOS: 109
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 31
;; LENGTH: 954
;; TYPE: PRT
;; ORGANISM: Arabidopsis thaliana
US-10-467-962B-31

Query Match 5.9%; Score 84.5; DB 6; Length 954;
Best Local Similarity 26.2%; Pred. No. 8.4;
Matches 34; Conservative 22; Mismatches 45; Indels 29; Gaps 6;

Qy 77 ICHLLKKKGYRCRTTEAEQDIEBEKVKIELND-----SVNNSDTVG--QIVHY 123

Db 785 LCSTLKVKAEDVTNRVENLLEELFAARKEASDLRSKAAVYKASVISNKAFTVGTSTIRV 844
Qy 124 IMK--NEANADVLKAMVAD--NSLYDPSTPTGSPV-----SPGPLSPGTPGK 173
Db 845 LVESMDTDDADSLKAAEHLSITLEDPAVVVLGSSPEKDKVSLVAATSPGVVSLGVQACK 904
Qy 174 HV-----CG 177
Db 905 FIGPIAKLCG 914

RESULT 11
US-11-072-512-2452
;; Sequence 2452, Application US/11072512
;; Publication No. US20060029945A1
;; GENERAL INFORMATION:
;; APPLICANT: ISOGAI, TAKAO
;; APPLICANT: SUGIYAMA, TOMOYASU
;; APPLICANT: OTSUKI, TETSUJI
;; APPLICANT: WAKAMATSU, AI
;; APPLICANT: SATO, HIROYUKI
;; APPLICANT: ISHII, SHIZUKO
;; APPLICANT: YAMAMOTO, JUN-ICHI
;; APPLICANT: ISONO, YUUKO
;; APPLICANT: HIO, YURI
;; APPLICANT: OTSUKA, KAORU
;; APPLICANT: NAGAI, KEIICHI
;; APPLICANT: IRIE, RYOTARO
;; APPLICANT: TAMECHIKA, ICHIRO
;; APPLICANT: YOSHIKAWA, TSUTOMU
;; APPLICANT: SEKI, NAOHICO
;; APPLICANT: OTSUKA, MOTOKYU
;; APPLICANT: NAGAHARI, KENJI
;; APPLICANT: MASUHO, YASUHIKO
;; TITLE OF INVENTION: Novel full length cDNA
;; FILE REFERENCE: 084335-0191
;; CURRENT APPLICATION NUMBER: US/11/072,512
;; CURRENT FILING DATE: 2005-03-07
;; PRIOR APPLICATION NUMBER: US 60/350,978
;; PRIOR FILING DATE: 2002-01-25
;; PRIOR APPLICATION NUMBER: JP 2001-379298
;; PRIOR FILING DATE: 2001-11-05
;; NUMBER OF SEQ ID NOS: 4096
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2452
;; LENGTH: 1344
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-072-512-2452

Query Match 5.9%; Score 84; DB 7; Length 1344;
Best Local Similarity 24.9%; Pred. No. 15;
Matches 53; Conservative 26; Mismatches 74; Indels 60; Gaps 12;

Qy 11 VLAAGV-FVGGAVSSPLVAPDNGSSRTLHSTRTTTPSPSNDTGNH-PEYIAYALVPVFF 68
Db 633 VLATTANWLPGLHSLPIC-----TTPKHYIRFGSPFIPERRRLLP--- 675
Qy 69 IMGLFGVLI CHLLK---KKGYRCRTTEAEQDIEBEKVKIELNDSVNSDTVGQIVHYIM 125
Db 676 -DGTFFSSCKRWIKQALEEGMTQTSVPQETRTQHLQ-----SNBNSSSS-----IC 723
Qy 126 KNEANADVLKAMVADNSLY-----DPESVPTPTGSPVSPGPLSPGCT-PCKH 174
Db 724 KD--NADLLSPLKKWKSRYLMEQNVTKLLRPLSPVTPPPNPSGSKSPQLATPGSSHGEE 781
Qy 175 VC--GHHL-----HTVGGVVERDVCHR 194
Db 782 ECRNGYSLMSPVTSLTASRCNTPLQFELCHR 814

RESULT 12

```

US-10-467-657-1672
;
; Sequence 1672, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1672
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1672

Query Match      5.8%; Score 82.5; DB 6; Length 399;
Best Local Similarity 25.4%; Pred. No. 3.9;
Matches 34; Conservative 15; Mismatches 58; Indels 27; Gaps 4;

QY 52 GNGHGPYIAVALVPVPFIM----GLFGVLICH-----LKKKGRCCTTEAEODI 96
DB 260 GPDPPCTYAEAVQKUMESKPIFGICLGHQLISLAIGAKTLKMRFSHGHAHPVQDL 319
QY 97 EEEKVEKIELNDVSNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPSPVTP--ST 154
DB 320 DSGKVVTITQNHGFAVDATL-----PANARITHKSLFDNTLQGIELTDKPVPCF 369
QY 155 PGSPVPVPGPLSPG 168
DB 370 QGHPEASPGQPDVG 383

RESULT 13
US-11-169-232-104
; Sequence 104, Application US/11169232
; Publication No. US20060025570A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Geener, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/169,232
; FILING DATE: 28-Jun-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991

US-10-467-657-1672
;
; Sequence 1672, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1672
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1672

Query Match      5.8%; Score 82.5; DB 6; Length 399;
Best Local Similarity 25.4%; Pred. No. 3.9;
Matches 34; Conservative 15; Mismatches 58; Indels 27; Gaps 4;

QY 52 GNGHGPYIAVALVPVPFIM----GLFGVLICH-----LKKKGRCCTTEAEODI 96
DB 260 GPDPPCTYAEAVQKUMESKPIFGICLGHQLISLAIGAKTLKMRFSHGHAHPVQDL 319
QY 97 EEEKVEKIELNDVSNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPSPVTP--ST 154
DB 320 DSGKVVTITQNHGFAVDATL-----PANARITHKSLFDNTLQGIELTDKPVPCF 369
QY 155 PGSPVPVPGPLSPG 168
DB 370 QGHPEASPGQPDVG 383

RESULT 13
US-11-169-232-104
; Sequence 104, Application US/11169232
; Publication No. US20060025570A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Geener, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/169,232
; FILING DATE: 28-Jun-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991

US-10-467-657-1672
;
; Sequence 1672, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1672
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1672

Query Match      5.8%; Score 82.5; DB 6; Length 399;
Best Local Similarity 25.4%; Pred. No. 3.9;
Matches 34; Conservative 15; Mismatches 58; Indels 27; Gaps 4;

QY 52 GNGHGPYIAVALVPVPFIM----GLFGVLICH-----LKKKGRCCTTEAEODI 96
DB 260 GPDPPCTYAEAVQKUMESKPIFGICLGHQLISLAIGAKTLKMRFSHGHAHPVQDL 319
QY 97 EEEKVEKIELNDVSNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPSPVTP--ST 154
DB 320 DSGKVVTITQNHGFAVDATL-----PANARITHKSLFDNTLQGIELTDKPVPCF 369
QY 155 PGSPVPVPGPLSPG 168
DB 370 QGHPEASPGQPDVG 383

RESULT 13
US-11-169-232-104
; Sequence 104, Application US/11169232
; Publication No. US20060025570A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Geener, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/169,232
; FILING DATE: 28-Jun-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991

US-10-467-657-1672
;
; Sequence 1672, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1672
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1672

Query Match      5.8%; Score 82.5; DB 6; Length 399;
Best Local Similarity 25.4%; Pred. No. 3.9;
Matches 34; Conservative 15; Mismatches 58; Indels 27; Gaps 4;

QY 52 GNGHGPYIAVALVPVPFIM----GLFGVLICH-----LKKKGRCCTTEAEODI 96
DB 260 GPDPPCTYAEAVQKUMESKPIFGICLGHQLISLAIGAKTLKMRFSHGHAHPVQDL 319
QY 97 EEEKVEKIELNDVSNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPSPVTP--ST 154
DB 320 DSGKVVTITQNHGFAVDATL-----PANARITHKSLFDNTLQGIELTDKPVPCF 369
QY 155 PGSPVPVPGPLSPG 168
DB 370 QGHPEASPGQPDVG 383

RESULT 13
US-11-169-232-104
; Sequence 104, Application US/11169232
; Publication No. US20060025570A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Geener, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/169,232
; FILING DATE: 28-Jun-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991

US-10-467-657-1672
;
; Sequence 1672, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1672
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1672

Query Match      5.8%; Score 82.5; DB 6; Length 399;
Best Local Similarity 25.4%; Pred. No. 3.9;
Matches 34; Conservative 15; Mismatches 58; Indels 27; Gaps 4;

QY 52 GNGHGPYIAVALVPVPFIM----GLFGVLICH-----LKKKGRC
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;
; FILING DATE: 28-Jun-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1363 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-11-169-232-52.

Query Match 5.8%; Score 82.5; DB 7; Length 1363;
Best Local Similarity 20.1%; Pred. No. 21;
Matches 55; Conservative 35; Mismatches 111; Indels 73; Gaps 9;

Qy 23 SSPLVAPDNGSSRTLHSTETTPSPNDTGNHPEYIAYALVPVFFIMGLFGVLICHLLK 82
Db 74 SSKAPPPGASQITKTKRSPKPPN-----100
Qy 83 KKGVCCTTEAQDIEEEKVEKIELNSVNSDVTGQI--VHYIMKNEANADVLKAM-VA 139
Db 101 KKTTKVIESEETEEHSVSENQESSSSSSSTIWKIKSSKNSAANRELQKLVK 160
Qy 140 DNSLYDPESPVTPTGSPVPVSPPLSPGG----TPGKHVCGHHLHTVGGVVERDVCHRC 195
Db 161 DNKKNRTKKKTPKPPVVDGAGSG-LDNGDPKVTTPDTSTTQHNKVSTSPKITT-----213
Qy 196 RHKRWHFIKPTNKSRSRPRRQGEVTVLSVGRFRVTKEHK-----SN 238
Db 214 -----AKPIN-PRPSLPNSDTSKETSLSLVNKETTETTKTTTNNKQTSDDGKEKTTTS 265
Qy 239 QKERRSLMSVSGAETV-NGEVPATPVKRSRGTE 271
Db 266 AKETQSIKTSKADLAPTSKVLAKPTPKAETTK 299

RESULT 15
US-11-169-232-2
; Sequence 2, Application US/11169232
; Publication No. US20060025570A1
; GENERAL INFORMATION:
; APPLICANT: Turner, Katherine
; Clark, Stephen C.
; Jacobs, Kenneth
; Hewick, Rodney M.
; Genser, Thomas G.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
```

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/169,232
; FILING DATE: 28-Jun-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-169-232-2

Query Match 5.8%; Score 82.5; DB 7; Length 1404;
Best Local Similarity 20.1%; Pred. No. 22;
Matches 55; Conservative 35; Mismatches 111; Indels 73; Gaps 9;

Qy 23 SSPLVAPDNGSSRTLHSTETTPSPNDTGNHPEYIAYALVPVFFIMGLFGVLICHLLK 82
Db 115 SSKAPPPGASQITKTKRSPKPPN-----141
Qy 83 KKGVCCTTEAQDIEEEKVEKIELNSVNSDVTGQI--VHYIMKNEANADVLKAM-VA 139
Db 142 KKTTKVIESEETEEHSVSENQESSSSSSSTIWKIKSSKNSAANRELQKLVK 201
Qy 140 DNSLYDPESPVTPTGSPVPVSPPLSPGG----TPGKHVCGHHLHTVGGVVERDVCHRC 195
Db 202 DNKKNRTKKKTPKPPVVDGAGSG-LDNGDPKVTTPDTSTTQHNKVSTSPKITT-----254
Qy 196 RHKRWHFIKPTNKSRSRPRRQGEVTVLSVGRFRVTKEHK-----SN 238
Db 255 -----AKPIN-PRPSLPNSDTSKETSLSLVNKETTETTKTTTNNKQTSDDGKEKTTTS 306
Qy 239 QKERRSLMSVSGAETV-NGEVPATPVKRSRGTE 271
Db 307 AKETQSIKTSKADLAPTSKVLAKPTPKAETTK 340
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Search completed: February 23, 2006, 12:12:39
Job time : 19 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 12:08:48 ; Search time 163 Seconds
(without alignments)
694.673 Million cell updates/sec

Title: US-10-620-562-2
Perfect score: 1426
Sequence: 1 MAPRALPGSAVLAIAAVFVGG.....ETVNGEVPATPVKRERSGTE 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1426	100.0	271	5	US-10-620-562-2
3	477.5	33.5	103	3	US-09-933-767-294
4	477.5	33.5	103	4	US-10-004-860-294
5	477.5	33.5	103	4	US-10-023-282-294
6	332	23.3	181	3	US-09-910-562-6
7	332	23.3	181	3	US-09-933-767-633
8	332	23.3	181	4	US-10-004-860-633
9	332	23.3	181	4	US-10-023-282-633
10	332	23.3	181	5	US-10-620-562-6
11	307	21.5	408	3	US-09-057-951-4
12	307	21.5	408	4	US-10-105-150-4
13	307	21.5	430	3	US-09-057-951-2
14	307	21.5	430	3	US-09-836-607-2
15	307	21.5	430	3	US-09-421-112-2
16	307	21.5	430	4	US-10-105-150-2
17	307	21.5	430	4	US-10-146-574-2
18	307	21.5	430	4	US-10-157-031-265
19	307	21.5	430	4	US-10-322-281-522
20	295.5	20.7	436	4	US-10-146-574-4
21	289.5	20.3	357	4	US-10-322-281-515
22	281	19.7	294	3	US-09-764-875-680
23	278.5	19.5	194	3	US-09-910-562-4
24	278.5	19.5	194	5	US-10-620-562-4
25	194	13.6	250	4	US-10-322-281-520
26	193.5	13.6	299	4	US-10-094-749-2913
27	147	10.3	29	3	US-09-910-562-7

28	147	10.3	29	3	US-09-933-767-634	Sequence 634, App
29	147	10.3	29	4	US-10-004-860-634	Sequence 634, App
30	147	10.3	29	4	US-10-023-282-634	Sequence 634, App
31	147	10.3	29	5	US-10-620-562-7	Sequence 7, Appli
32	131	9.2	66	3	US-09-796-692-1534	Sequence 1534, Ap
33	131	9.2	66	4	US-10-040-862-1534	Sequence 1534, Ap
34	131	9.2	66	4	US-10-057-475B-1534	Sequence 1534, Ap
35	131	9.2	66	4	US-10-154-884B-1534	Sequence 1534, Ap
36	131	9.2	66	4	US-10-764-324-1534	Sequence 1534, Ap
37	114	8.0	96	4	US-10-322-281-518	Sequence 518, App
38	102.5	7.2	1829	4	US-10-437-963-192144	Sequence 192144,
39	97.5	6.8	447	4	US-10-104-047-2688	Sequence 2688, Ap
40	97.5	6.8	1049	5	US-10-487-561-80	Sequence 80, Appli
41	97.5	6.8	1513	4	US-10-369-493-19093	Sequence 19093, A
42	97.5	6.8	1746	4	US-10-220-955-17	Sequence 17, Appli
43	97	6.8	287	4	US-10-290-631-6	Sequence 6, Appli
44	97	6.8	287	4	US-10-290-631-8	Sequence 8, Appli
45	97	6.8	287	4	US-10-777-524-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-910-562-2
; Sequence 2, Application US/09910562
; Patent No. US20020098163A1
; GENERAL INFORMATION:
; APPLICANT: Zeng et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptors TR21 and TR22
; FILE REFERENCE: PF530
; CURRENT APPLICATION NUMBER: US/09/910,562
; PRIOR FILING DATE: 2001-07-23
; PRIOR FILING DATE: 2000-07-27
; PRIOR FILING DATE: 2000-07-27
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 271
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-910-562-2

Query Match	100.0%;	Score 1426;	DB 3;	Length 271;
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Matches 271;	Conservative 0;			
Qy	1	MAPRALPGSAVLAIAAVFVGGAVSSPLVAPDNGSSRTLHSRTTETTPSPSNDTGNHGPYIA	60	
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Qy	61	YALVPVFFIMGLFGVLICHLLKKGYRCCTTEAEODIBEEKVEKIELDNDVNSDVTVCQI	120	
Db	61	YALVPVFFIMGLFGVLICHLLKKGYRCCTTEAEODIBEEKVEKIELDNDVNSDVTVCQI	120	
Qy	121	VHYIMKNEADVLKAMVADNSLYDPSVTPSPGSPVPSPGSPGTPGKVCGHHL	180	
Db	121	VHYIMKNEADVLKAMVADNSLYDPSVTPSPGSPVPSPGSPGTPGKVCGHHL	180	
Qy	181	HTVGVVVERDVCHCRHWRHFIKPTNKSRESRRRQGEVTVLSVGRFRVTKEVHKSNOK	240	
Db	181	HTVGVVVERDVCHCRHWRHFIKPTNKSRESRRRQGEVTVLSVGRFRVTKEVHKSNOK	240	
Qy	241	ERRSLMSVSGAETVNGEVPATPVKRERSGTE	271	
Db	241	ERRSLMSVSGAETVNGEVPATPVKRERSGTE	271	
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US-10-620-562-2				
; Sequence 2, Application US/10620562				

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/ Publication No. US20050090436A1
/ GENERAL INFORMATION:
/ APPLICANT: Zeng, Z et al.
/ TITLE OF INVENTION: Human Tumor Necrosis Factor receptors TR21 and TR22
/ FILE REFERENCE: PF530C1
/ CURRENT APPLICATION NUMBER: US/10/620,562
/ CURRENT FILING DATE: 2003-07-17
/ PRIOR APPLICATION NUMBER: 09/910,562
/ PRIOR FILING DATE: 2001-07-23
/ PRIOR APPLICATION NUMBER: 60/221,143
/ PRIOR FILING DATE: 2000-07-27
/ PRIOR APPLICATION NUMBER: 60/220,116
/ PRIOR FILING DATE: 2000-07-24
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 271
/ TYPE: PRT
/ ORGANISM: homo sapiens
/ ORGANISM: homo sapiens
US-10-620-562-2

Query Match 100.0%; Score 1426; DB 5; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.4e-118;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAPRALPGSAVLAAPVGVGAVSPPLVAPDNGSSRTLHSRTTTPSPSNDTGNGHPEYIA 60
QY 61 YALVPVFFIMGLFGLVILCHLLKKKGKRCCTTAEQDIEEEKVEKIELNDSVNENS DTVGQI 120
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QY 121 VHYIMKNEANADVLKAMVADNSLYDPSPVTPSTPGSPPPVSPGSPGTPGKHVCGHHL 180
Db 121 VHYIMKNEANADVLKAMVADNSLYDPSPVTPSTPGSPPPVSPGSPGTPGKHVCGHHL 180
QY 181 HTVGGVVERDVCHRCRKHWHFKPTNKSRSPRQGEVTVLSVGRFRTVKVEHKSNOK 240
Db 181 HTVGGVVERDVCHRCRKHWHFKPTNKSRSPRQGEVTVLSVGRFRTVKVEHKSNOK 240
QY 241 ERRLMSVSGAETVNGEVPATPVKRRERSGTE 271
Db 241 ERRLMSVSGAETVNGEVPATPVKRRERSGTE 271

RESULT 3
US-09-933-767-294
/ Sequence 294, Application US/099333767
/ Publication No. US20030181692A1
/ GENERAL INFORMATION:
/ APPLICANT: Ni et al.
/ TITLE OF INVENTION: 207 Human Secreted Proteins
/ FILE REFERENCE: P2007P2
/ CURRENT APPLICATION NUMBER: US/09/933,767
/ CURRENT FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: PCT/US01/05614
/ PRIOR FILING DATE: 2001-02-21
/ PRIOR APPLICATION NUMBER: 60/184,836
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 60/193,170
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: 09/205,258
/ PRIOR FILING DATE: 1998-12-04
/ PRIOR APPLICATION NUMBER: PCT/US98/11422
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/048,885
/ PRIOR FILING DATE: 1997-06-06
/ PRIOR APPLICATION NUMBER: 60/049,375
/ PRIOR FILING DATE: 1997-06-06
/ PRIOR APPLICATION NUMBER: 60/048,881
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/ PRIOR APPLICATION NUMBER: 60/048,880
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/ PRIOR APPLICATION NUMBER: 60/049,020
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/ PRIOR APPLICATION NUMBER: 60/048,876
/ PRIOR FILING DATE: 1997-06-06
/ PRIOR APPLICATION NUMBER: 60/048,895
/ PRIOR FILING DATE: 1997-06-06
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/ PRIOR FILING DATE: 1997-06-06
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/ PRIOR FILING DATE: 1997-06-06
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/ PRIOR FILING DATE: 1997-06-06
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/ PRIOR FILING DATE: 1997-06-06
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/ PRIOR FILING DATE: 1997-06-06
/ PRIOR APPLICATION NUMBER: 60/068,054
/ PRIOR FILING DATE: 1997-12-18
/ PRIOR APPLICATION NUMBER: 60/068,064
/ PRIOR FILING DATE: 1997-12-18
/ PRIOR APPLICATION NUMBER: 60/068,053
/ PRIOR FILING DATE: 1997-12-18
/ PRIOR APPLICATION NUMBER: 60/070,923
/ PRIOR FILING DATE: 1997-12-18
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; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 294
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (78)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (80)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (81)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (103)
; OTHER INFORMATION: Xaa equals stop translation
; US-09-333-767-294

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Best Local Similarity 95.0%; Pred. No. 2e-34;
Matches 96; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (78)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (80)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (81)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (103)
; OTHER INFORMATION: Xaa equals stop translation
; US-10-004-860-294

Query Match          33.5%; Score 477.5; DB 4; Length 103;
Best Local Similarity 95.0%; Pred. No. 2e-34;
Matches 96; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Db 1 MAPRALPGSAVLAAAVFGGAVSSPLVAPDNGSSRTLHSRTTTPSPSNDTGNHPEYIA 60
Qy 61 YALVPVFFIMGLFGVLIC-HLLKKKGRCYCTTEAQDIEEK 100
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RESULT 5
US-10-023-282-294
; Sequence 294, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
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; EARLIER APPLICATION NUMBER: 60/048,876
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; EARLIER APPLICATION NUMBER: 60/048,895
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; EARLIER APPLICATION NUMBER: 60/048,964

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; PRIOR FILING DATE: 1998-01-30
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; PRIOR APPLICATION NUMBER: 60/085,922
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; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
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; SEQ ID NO 294
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (78)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (80)
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; NAME/KEY: SITE
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; LOCATION: (103)
; OTHER INFORMATION: Xaa equals stop translation
; US-09-333-767-294

Query Match          33.5%; Score 477.5; DB 3; Length 103;
Best Local Similarity 95.0%; Pred. No. 2e-34;
Matches 96; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 MAPRALPGSAVLAAAVFGGAVSSPLVAPDNGSSRTLHSRTTTPSPSNDTGNHPEYIA 60
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Db 61 YALVPVFFIMGLFGVLIXPXXXXKKGYRCTTEAQDIEEK 101

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; Sequence 294, Application US/10004860
; Publication No. US20030065160A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 294
LENGTH: 103
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (78)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (80)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (81)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:
NAME/KEY: SITE
LOCATION: (82)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (103)
OTHER INFORMATION: Xaa equals stop translation
US-10-023-282-294
Query Match 33.5%; Score 477.5; DB 4; Length 103;
Best Local Similarity 95.0%; Pred. No. 2e-34;
Matches 96; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 MAPRALPGSAVLAANAVFVGAVSSPLVAPDNGSSRTLHSTETTPSPSNDTGNCHPEYIA 60
DB 1 MAPRALPGSAVLAANAVFVGAVSSPLVAPDNGSSRTLHSTETTPSPSNDTGNCHPEYIA 60
QY 61 YALVPVFFIMGLFGLVIC-HLLKKKGRCYCTTEAEQDIEEEK 100
DB 61 YALVPVFFIMGLFGLVIC-PPXXXXKKGYRCYCTTEAEQDIEEEK 101
RESULT 6
US-09-910-562-6
Sequence 6, Application US/09910562
Patent No. US20020098163A1
GENERAL INFORMATION:
APPLICANT: Zeng et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptors TR21 and TR22
FILE REFERENCE: PF530
CURRENT APPLICATION NUMBER: US/09/910,562
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 60/221,143
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/220,116
PRIOR FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 181
TYPE: PRT
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (56)..(57)
OTHER INFORMATION: Xaa equals any amino acid
NAME/KEY: SITE
LOCATION: (60)..(60)
OTHER INFORMATION: Xaa equals any amino acid
NAME/KEY: SITE
LOCATION: (83)..(84)
OTHER INFORMATION: Xaa equals any amino acid
NAME/KEY: SITE
LOCATION: (165)..(165)
OTHER INFORMATION: Xaa equals any amino acid
US-09-910-562-6
Query Match 23.3%; Score 332; DB 3; Length 181;
Best Local Similarity 85.5%; Pred. No. 3.6e-21;
Matches 65; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 97 EEEKVEKIELNDSVNSDVTGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPG 156
DB 76 KKKKFKKXKLNDSVNSDVTGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPG 135
QY 157 SPPVSPGLSPGCTPG 172
DB 136 SPPVSPGLCHQGRQG 151
RESULT 7
US-09-933-767-633

; Sequence 633, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949

; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,897
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,898
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 633
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (56)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (57)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (83)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (165)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-933-767-633

Query Match 23.3%; Score 332; DB 3; Length 181;

EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 633
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (56)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (60)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (57)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (83)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (84)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (165)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-023-282-633

Query Match 23.3%; Score 332; DB 4; Length 181;
Best Local Similarity 85.5%; Pred. No. 3.6e-21;
Matches 65; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 97 EEKVEKIELDLSVNSDVTGQIVHYIMKNEANADVLKAMVADNSLYDPSPVTPSTPG 156
Db 76 KKKKVEKKXLNDSVNSDVTGQIVHYIMKNEANADVLKAMVADNSLYDPSPVTPSTPG 135

Qy 157 SPVSPGCLSPGGTGP 172
Db 136 SPVSPGCLCHQGGGQQ 151

RESULT 10
US-10-620-562-6
Sequence 6, Application US/10620562
Publication No. US20050090436A1
GENERAL INFORMATION:
APPLICANT: Zeng, Z et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor receptors TR21 and TR22
FILE REFERENCE: PF530C1
CURRENT APPLICATION NUMBER: US/10/620,562
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 09/910,562
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 60/221,143
PRIOR FILING DATE: 2000-07-27

PRIOR APPLICATION NUMBER: 60/220,116
PRIOR FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 181
TYPE: PRT
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (56)-(57)
OTHER INFORMATION: X equals any amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (60)-(60)
OTHER INFORMATION: X equals any amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (83)-(84)
OTHER INFORMATION: X equals any amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (165)-(165)
OTHER INFORMATION: X equals any amino acid
US-10-620-562-6

Query Match 23.3%; Score 332; DB 5; Length 181;
Best Local Similarity 85.5%; Pred. No. 3.6e-21;
Matches 65; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 97 EEKVEKIELDLSVNSDVTGQIVHYIMKNEANADVLKAMVADNSLYDPSPVTPSTPG 156
Db 76 KKKKVEKKXLNDSVNSDVTGQIVHYIMKNEANADVLKAMVADNSLYDPSPVTPSTPG 135

Qy 157 SPVSPGCLSPGGTGP 172
Db 136 SPVSPGCLCHQGGGQQ 151

RESULT 11
US-09-057-951-4
Sequence 4, Application US/09057951
Patent No. US20020025551A1
GENERAL INFORMATION:
APPLICANT: Holzman, Douglas
TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq For Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,951
FILING DATE: 09-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Weiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

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/ ; LENGTH: 408 amino acids
/ ; TYPE: amino acid
/ ; TOPOLOGY: linear
/ ; MOLECULE TYPE: protein
US-09-057-951-4

Query Match      21.5%; Score 307; DB 3; Length 408;
Best Local Similarity 31.0%; Pred. No. 1.8e-18;
Matches 84; Conservative 36; Mismatches 69; Indels 82; Gaps 12;

QY 44 TPSPSNDTGNHPE-----YIAVALVPVFFIMGLFGVLICHLKKKGYRCTTEAE----- 93
Db 122 TROPNGNTRAGGPEETAQAQAVIAIVPVFCMLGILLVCNLLKRGYHCTAHKEVGP 181
QY 94 -----QDIEEEKVEKIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVAD 140
Db 182 GGGGGINPAYRTED-----ANEDTIGVLRLITEKKENAAALEELLKE 225
QY 141 NSLYDPESPVTPSPGPPVSPGSPGTPGKHVC--GHHLHTVGV--VERDVCCHRCR 196
Db 226 ---YHSKQLVQTS---HRPVSKLPPAPPNPV--HICPHRHLLHTVQGLASLSGPPCCSRCS 277
QY 197 HKWHFI-----KPTNKSRE--SRPRQGEVTVLSVGRFRVTKVHKHS 237
Db 278 QKKWPEVLLSPEAVAATTVPVSLLPNPTRVPKAKAGAGROGEITILSVGRFRVARI---- 333
QY 238 NOKERSLSMSVSGAETVN-----GEVPATP 262
Db 334 --PEQRTSSMVSEVKTTITEAGPSWGDLPDSP 362

RESULT 12
US-10-105-150-4
; Sequence 4, Application US/10105150
; Publication No. US20020119524A1
; GENERAL INFORMATION:
; APPLICANT: Holzman, Douglas
; TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/105,150
; FILING DATE: 25-Mar-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/057,951
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/046001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-105-150-4
Query Match      21.5%; Score 307; DB 4; Length 408;
Best Local Similarity 31.0%; Pred. No. 1.8e-18;
Matches 84; Conservative 36; Mismatches 69; Indels 82; Gaps 12;

QY 44 TPSPSNDTGNHPE-----YIAVALVPVFFIMGLFGVLICHLKKKGYRCTTEAE----- 93
Db 122 TROPNGNTRAGGPEETAQAQAVIAIVPVFCMLGILLVCNLLKRGYHCTAHKEVGP 181
QY 94 -----QDIEEEKVEKIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVAD 140
Db 182 GGGGGINPAYRTED-----ANEDTIGVLRLITEKKENAAALEELLKE 225
QY 141 NSLYDPESPVTPSPGPPVSPGSPGTPGKHVC--GHHLHTVGV--VERDVCCHRCR 196
Db 226 ---YHSKQLVQTS---HRPVSKLPPAPPNPV--HICPHRHLLHTVQGLASLSGPPCCSRCS 277
QY 197 HKWHFI-----KPTNKSRE--SRPRQGEVTVLSVGRFRVTKVHKHS 237
Db 278 QKKWPEVLLSPEAVAATTVPVSLLPNPTRVPKAKAGAGROGEITILSVGRFRVARI---- 333
QY 238 NOKERSLSMSVSGAETVN-----GEVPATP 262
Db 334 --PEQRTSSMVSEVKTTITEAGPSWGDLPDSP 362

RESULT 13
US-09-057-951-2
; Sequence 2, Application US/09057951
; Patent No. US2002002551A1
; GENERAL INFORMATION:
; APPLICANT: Holzman, Douglas
; TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,951
; FILING DATE: 09-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/046001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-057-951-2

Query Match      21.5%; Score 307; DB 3; Length 430;
Best Local Similarity 31.0%; Pred. No. 1.9e-18;
Matches 84; Conservative 36; Mismatches 69; Indels 82; Gaps 12;

QY 44 TPSPSNDTGNHPE-----YIAVALVPVFFIMGLFGVLICHLKKKGYRCTTEAE----- 93
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Db 144 TROPNGTRAGGPEETAQAQYAVIAIVFVFCIMGLGILVNCNLLKRGYHCTAHKEVGGP 203
Qy 94 -----QDIEEEKVEKIELNDSVNENSNTVGVQIVHYIMKNEANADVLKAMVAD 140
Db 204 GGGGGINPAYRTED-----ANEDTIGVLVRLITEKKENAAALELLKE 247
Qy 141 NSLYDPESPVTPTSGSPVPGPLSPGTPGKHVC--GHHLHTVGV--VERDVCHRCR 196
Db 248 ---YHSKQLVQTS---HRPVSKLPPAPPNPV--HICPHRHLLHTVQGLASLSGPCSCS 299
Qy 197 HKRWHTF-----KPTNKSRE--SRPRROGEVTVLSVGRFVTKVEHKS 237
Db 300 QKKWPEVLLSPEAVAATTPVPSLLPNPTRVPKAKAGRQGEITILSVGRFVRARI---- 355
Qy 238 NQKERRSLMSVSGAETVN-----GEVPATP 262
Db 356 --PEQRTSSMVSEVKTITEAGPSWGDLPDSP 384

RESULT 14

US-09-836-607-2
; Sequence 2, Application US/09836607
; Patent No. US20020098541A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: TNFR Related Gene 12
; FILE REFERENCE: PE490P1
; CURRENT APPLICATION NUMBER: US/09/836,607
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/198,388
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 09/421,112
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,950
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-607-2

Query Match 21.5%; Score 307; DB 3; Length 430;
Best Local Similarity 31.0%; Pred. No. 1.9e-18;
Matches 84; Conservative 36; Mismatches 69; Indels 82; Gaps 12;
Qy 44 TSPSNDTGNHPE-----YIAVALPVFFIMGLFGLVLIHLLKKGYRCTTEAE----- 93
Db 144 TROPNGTRAGGPEETAQAQYAVIAIVFVFCIMGLGILVNCNLLKRGYHCTAHKEVGGP 203
Qy 94 -----QDIEEEKVEKIELNDSVNENSNTVGVQIVHYIMKNEANADVLKAMVAD 140
Db 204 GGGGGINPAYRTED-----ANEDTIGVLVRLITEKKENAAALELLKE 247
Qy 141 NSLYDPESPVTPTSGSPVPGPLSPGTPGKHVC--GHHLHTVGV--VERDVCHRCR 196
Db 248 ---YHSKQLVQTS---HRPVSKLPPAPPNPV--HICPHRHLLHTVQGLASLSGPCSCS 299
Qy 197 HKRWHTF-----KPTNKSRE--SRPRROGEVTVLSVGRFVTKVEHKS 237
Db 300 QKKWPEVLLSPEAVAATTPVPSLLPNPTRVPKAKAGRQGEITILSVGRFVRARI---- 355
Qy 238 NQKERRSLMSVSGAETVN-----GEVPATP 262
Db 356 --PEQRTSSMVSEVKTITEAGPSWGDLPDSP 384

RESULT 15

US-09-421-112-2
; Sequence 2, Application US/09421112

; Publication No. US20030082532A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: TNFR Related Gene 12
; FILE REFERENCE: PE490
; CURRENT APPLICATION NUMBER: US/09/421,112
; CURRENT FILING DATE: 1999-10-19
; EARLIER APPLICATION NUMBER: 60/104,950
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-421-112-2

Query Match 21.5%; Score 307; DB 3; Length 430;
Best Local Similarity 31.0%; Pred. No. 1.9e-18;
Matches 84; Conservative 36; Mismatches 69; Indels 82; Gaps 12;
Qy 44 TSPSNDTGNHPE-----YIAVALPVFFIMGLFGLVLIHLLKKGYRCTTEAE----- 93
Db 144 TROPNGTRAGGPEETAQAQYAVIAIVFVFCIMGLGILVNCNLLKRGYHCTAHKEVGGP 203
Qy 94 -----QDIEEEKVEKIELNDSVNENSNTVGVQIVHYIMKNEANADVLKAMVAD 140
Db 204 GGGGGINPAYRTED-----ANEDTIGVLVRLITEKKENAAALELLKE 247
Qy 141 NSLYDPESPVTPTSGSPVPGPLSPGTPGKHVC--GHHLHTVGV--VERDVCHRCR 196
Db 248 ---YHSKQLVQTS---HRPVSKLPPAPPNPV--HICPHRHLLHTVQGLASLSGPCSCS 299
Qy 197 HKRWHTF-----KPTNKSRE--SRPRROGEVTVLSVGRFVTKVEHKS 237
Db 300 QKKWPEVLLSPEAVAATTPVPSLLPNPTRVPKAKAGRQGEITILSVGRFVRARI---- 355
Qy 238 NQKERRSLMSVSGAETVN-----GEVPATP 262
Db 356 --PEQRTSSMVSEVKTITEAGPSWGDLPDSP 384

Search completed: February 23, 2006, 12:12:15
Job time : 164 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 12:08:03 ; Search time 47 Seconds
(without alignments)
476.704 Million cell updates/sec

Title: US-10-620-562-2

Perfect score: 1426

Sequence: 1 MAPRALPGSAVLAANFVGG.....ETVNGEVPATPVKRSRGTE 271

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
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 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	477.5	33.5	103	2	US-09-205-258-294
2	477.5	33.5	103	2	US-10-004-860-294
3	332	23.3	181	2	US-09-205-258-633
4	332	23.3	181	2	US-10-004-860-633
5	282	19.8	518	2	US-09-949-016-10986
6	147	10.3	29	2	US-09-205-258-634
7	147	10.3	29	2	US-10-004-860-634
8	103.5	7.3	819	2	US-09-248-796A-15758
9	97.5	6.8	447	2	US-10-104-047-2688
10	97	6.8	287	2	US-08-985-950-6
11	97	6.8	287	2	US-08-985-950-8
12	97	6.8	287	2	US-09-546-049-6
13	97	6.8	287	2	US-09-546-049-8
14	95	6.7	992	2	US-08-890-865A-1
15	94	6.6	793	1	US-08-015-985-3
16	94	6.6	793	2	US-09-280-597-3
17	92.5	6.5	591	2	US-09-248-796A-14242
18	91.5	6.4	527	2	US-09-370-838-216
19	91.5	6.4	527	2	US-09-854-133-216
20	90.5	6.3	8991	2	US-08-714-741-32
21	89.5	6.3	901	2	US-09-828-062-8
22	89	6.2	401	1	US-08-549-004A-5
23	89	6.2	401	2	US-09-051-982A-5
24	89	6.2	605	2	US-09-487-558B-428
25	88	6.2	330	2	US-09-270-767-41611
26	88	6.2	539	2	US-08-906-360-1
27	87.5	6.1	559	2	US-08-956-171E-5251

28	87.5	6.1	559	2	US-08-781-986A-5251
29	87.5	6.1	1420	1	US-08-540-804-14
30	87.5	6.1	1420	1	US-08-218-265-14
31	87.5	6.1	1420	2	US-08-521-872-14
32	87.5	6.1	1420	2	US-08-590-399-14
33	87.5	6.1	1420	2	US-08-487-558B-356
34	87	6.1	761	2	US-09-198-452A-335
35	87	6.1	902	2	US-09-438-185A-319
36	86.5	6.1	290	2	US-09-270-767-35246
37	86.5	6.1	290	2	US-09-270-767-50463
38	86	6.0	204	2	US-08-529-055-51
39	86	6.0	547	2	US-08-221-013A-14
40	86	6.0	729	2	US-09-949-016-11190
41	86	6.0	2753	2	US-09-949-016-7659
42	86	6.0	2753	2	US-09-949-016-7660
43	86	6.0	3924	2	US-09-538-092-1246
44	85.5	6.0	168	2	US-08-529-055-55
45	85.5	6.0	183	2	US-08-529-055-50

ALIGNMENTS

RESULT 1
US-09-205-258-294
; Sequence 294, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
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; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06

Sequence 5251, Ap
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Sequence 356, Appl
Sequence 335, Appl
Sequence 319, Appl
Sequence 35246, A
Sequence 50463, A
Sequence 51, Appl
Sequence 14, Appl
Sequence 11190, A
Sequence 7659, Ap
Sequence 7660, Ap
Sequence 1246, Ap
Sequence 55, Appl
Sequence 50, Appl


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; EARLIER APPLICATION NUMBER: 60/049,375
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; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
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; EARLIER APPLICATION NUMBER: 60/048,916
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; EARLIER APPLICATION NUMBER: 60/049,373
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; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18

; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 633
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (56)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
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; NAME/KEY: SITE
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; NAME/KEY: SITE
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; NAME/KEY: SITE
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-205-258-633

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Best Local Similarity 85.5%; Pred. No. 1.6e-25;
Matches 65; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 97 EEKVKELIENLSDVNSNSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPSVTPSTPG 156
Db 76 KKKKVEKXLDNSVNSNSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPSVTPSTPG 135
Qy 157 SPVSPGLSPGSGTGG 172
Db 136 SPVSPGLCHGGRQG 151

RESULT 4
US-10-004-860-633
; Sequence 633, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 633
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (56)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (57)
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; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 634
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-634

Query Match 10.3%; Score 147; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 IMKNEANADVLMKAMVADNSLYDPSPVTP 152
Db 1 IMKNEANADVLMKAMVADNSLYDPSPVTP 29

RESULT 7

US-10-004-860-634
; Sequence 634, Application US/10004860
; Patent No. 6314047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 634
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-004-860-634

Query Match 10.3%; Score 147; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 IMKNEANADVLMKAMVADNSLYDPSPVTP 152
Db 1 IMKNEANADVLMKAMVADNSLYDPSPVTP 29

RESULT 8

US-09-248-796A-15758
; Sequence 15758, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15758
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15758

Query Match 7.3%; Score 103.5; DB 2; Length 819;
Best Local Similarity 27.1%; Pred. No. 0.19;
Matches 26; Conservative 21; Mismatches 38; Indels 11; Gaps 2;
QY 91 EAEQDIEEEKVEKIELNDSVNSDVTGQIVHYIMKNEANADVLMKAMVADNSLYDPSPV 150
Db 721 DKDEDKDKDEEDDDDEYNDENEDTDELV-----AGFEKVVLPTEDKSMGTSPSPFI 773
QY 151 TPSTPGSP-----VSPGFLSPGGTTPGRKHVCGHHLHT 182
Db 774 IPSTPKTPTSITPTTSKSTTTTITASTETIGKRLST 809

RESULT 9

US-10-104-047-2688
; Sequence 2688, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2688
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2688

Query Match 6.8%; Score 97.5; DB 2; Length 447;
Best Local Similarity 20.6%; Pred. No. 0.32;
Matches 72; Conservative 37; Mismatches 87; Indels 153; Gaps 16;

QY 29 PDNGSSRTH-----SRTEPPSPNDTNGHPPEYI 59
Db 73 PDNTSKTDTCLQTKGFSNSTEHRGSAQKVQEFNNCLNRGQSSPQRSYSSSHSSPAKI 132
QY 60 AYALVPVFFPFLGVLICHLLKKGYRCTTEAEQDIEEEKVEKIELNDSVNSDVT-G 118
Db 133 -----QRATQEPVAKIEGTQESQMVGSSSTREKASTVLS 166
QY 119 QIVHYIMKNEA-----NADVLMKAM-----VADNSLY----- 144
Db 167 QIVASTQPPQSPPETPQSGPKACSVELYAIIPDADAVAKSTPKSTPVRKSLFTSQSPGE 226
QY 145 -----DPE-SPVTPS-----TFGSPVSPGFLSPGGTTPGRKHVCGHHLH 181
Db 227 AEAPQITDSTPTTKVQKQPSIKPVTSPSKLVTSPQSEPPAPP-PPRSTSSPYHAGNLLQ 285
QY 182 TVGGVVERDVCHRCRH-KRWHF1KPTNKS-----ESPRRQGEVTVL 223
Db 286 -----RHPTNW--TKPTSPTSTAEASVLSHSGSRRAADAKPKRW--ISFK 327

Qy	224	SVGRFRVTKVE-HKSNQKERRSLMSVSGAETVNGEVPATPVKRRSGTE	271
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D _b	328	SFFRRKTDDEDDKEKEREKGLVGLDG--TVIHLPPPPVORHHWTFE	374
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Query Match	6.8%	Score 97;	DB 2;	Length 287;
Best Local Similarity	22.7%;	Pred. No.	0.19;	
Matches	58;	Conservative	45;	Mismatches 105; Indels 48; Gaps 14;
Qy	34	SRTLHSRTETTPSSNDTGNCHPEYIAVALVPV----	FFIMGLFGVLICHLLMKKGVC	88
		:::::	:::::	:::::
Db	16	AQIHTQEEDLPRPSISAEPC-----	TVIPGSHVTFCRGPVGQTFRLERES--RS	66
Qy	89	TTRABQDIBEEKVEKIELN---DSVNENSDTVGOIVHY-	IMKNKANADVLKAMWADNSLY	144
		:::::	:::::	:::::
Db	67	TYNDTEDVSOAPSSESARFRIDSVSEGNAGPYRCIIYKPP	KWSEQSDYLELLVKETS-G	125
Qy	145	DPSPTV-PTPGSPPVSP-----	GPLSPGGTGPCKHVCGHHLHTWGCV-VERDVCHR	194
		:::::	:::::	:::::
Db	126	GPSDPTEPSSSAGTORPDNSHNEAPASQG-----	LKAELHYLIIGUSVVVFCLL	179
Qy	195	-----CHKRWHFTK----PTNKSRSPRRQGEVTV----	LSVGRFRTKVKEHKSNOKER	242
Db	180	LLVFLCLH-RQNQIKOGPPRSKDREQPOPDLAVDLBARTAD	KATVNGLPKEDRETDT	238

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Qy      243 RSLMSVSGAETNGEV 258
       :|:| |
Db      239 SALAAGSSQEVTYAQL 254

RESULT 11
US-08-985-950-8
; Sequence 8, Application US/08985950
; Patent NO. 6140076
; GENERAL INFORMATION:
; APPLICANT: Adena, Gorse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; JS-08-985-950-8

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[illegible]

Qy 243 RSLMSVSGAETVNGEV 258
Db 239 SALAAGSSQEVTYAQL 254

RESULT 12
US-09-546-049-6
; Sequence 6, Application US/09546049
; Patent No. 6479638
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; Meyaard, Linde
; Gorman, Daniel M.
; McClanahan, Terrill K.
; Zurawski, Sandra M.
; Zurawski, Gerard
; Lanier, Lewis L.
; Phillips Jr., Joseph H.
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; Related Reagents
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/546,049
; FILING DATE: 10-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1204
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-546-049-6

Query Match 6.8%; Score 97; DB 2; Length 287;
Best Local Similarity 22.7%; Pred. No. 0.19;
Matches 56; Conservative 45; Mismatches 105; Indels 48; Gaps 14;

Qy 34 SRLHSRTETPPSNDTGNHGYIAYALVPV-----FTIMGLFGVLICHLLKKGKGYRC 88
Db 16 AQTIHQEEDLPRFSIAEPG-----TWIPLGSHVTFVCRGPVGVTFLERES--RS 66

Qy 89 TTEAQDIEBKVKIELN---DSVNSDSTVGQIVHY-IMKNEANADVLKAMVADNSLY 144
Db 67 TYNDTVDVSQASPESEARFIDSVSEGNAGPYRCIYKPKKWEQSDYLELLVKETS-G 125

Qy 145 DPESPVT-PSTPGSPVPVSP-----GPLSPGTPGKHVCGHHLHTVGGV-VERDVCHR 194
Db 126 GPDSPTPEGSGAGPTQRPDSNDSHNEHAPASQG-----LKAELHYILIGSVVFLFCLL 179

Qy 195 -----CRHKEWHFK---PTNKSRESRPRGGEVTV-----LSVGRFRVTKVHEKSNOKER 242
Db 180 LLVLFCLH-RQNIKQGPSPKDEEQPQRPDLAVDLVLTADKATVNGLPKSDREYDT 238

Qy 243 RSLMSVSGAETVNGEV 258
Db 239 SALAAGSSQEVTYAQL 254

RESULT 13
US-09-546-049-8
; Sequence 8, Application US/09546049
; Patent No. 6479638
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; Meyaard, Linde
; Gorman, Daniel M.
; McClanahan, Terrill K.
; Zurawski, Sandra M.
; Zurawski, Gerard
; Lanier, Lewis L.
; Phillips Jr., Joseph H.
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; Related Reagents
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/546,049
; FILING DATE: 10-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1204
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 287 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-546-049-8

Query Match 6.8%; Score 97; DB 2; Length 287;
Best Local Similarity 22.7%; Pred. No. 0.19;
Matches 58; Conservative 45; Mismatches 105; Indels 48; Gaps 14;

Db	318	M W E Q T A T V M T N L K E K E C A Q W P D Q C W T Y G N V R V S V E D V T V L V D Y T V R K F S I Q	377
Qy	232	K V E H K S N Q K E R R S L M S V S G A E T V N G E V P A T E V	263
Db	378	Q V G D V T N R K P Q R L I T Q F H T S W P D F G V P F T E I	409

Search completed: February 23, 2006, 12:09:26
Job time : 48 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 12:00:48 ; Search time 231 Seconds
(without alignments)
827.698 Million cell updates/sec

Title: US-10-620-562-2

Perfect score: 1426

Sequence: 1 MAPRALPGSAVLAFAVFGG.....ETVNGSVPTPVKRSRGTE 271

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1426	100.0	271	2	Q8IUW5 HUMAN
2	1421	99.6	271	2	Q8NKK1 HUMAN
3	986	69.1	202	2	Q8K2J7 MOUSE
4	854.5	59.9	288	2	Q5F3A4 CHICK
5	699	49.0	143	2	Q8R3S5 MOUSE
6	669	46.9	223	2	Q7T0N2 XENLA
7	641.5	45.0	224	2	Q6NRQ3 XENLA
8	581	40.7	280	2	Q5M7X6 BRARE
9	422.5	29.6	281	2	Q4SRN7 TETNG
10	309	21.7	430	1	TR19L MACFA
11	307	21.5	430	1	TR19L HUMAN
12	295.5	20.7	436	1	TR19L MOUSE
13	289	20.3	294	2	Q8CFT0 MOUSE
14	289	20.3	303	2	Q8BRJ3 MOUSE
15	289	20.3	325	2	Q6DIW4 XENTR
16	286	20.1	302	2	Q5FVJ4 RAT
17	286	20.1	327	2	Q68EV2 XENLA
18	284	19.9	303	2	Q6P4E7 HUMAN
19	284	19.9	303	2	Q6UXY2 HUMAN
20	284	19.9	303	2	Q8NC24 HUMAN
21	282.5	19.8	401	2	Q6N211 BRARE
22	158.5	11.1	163	2	Q4SEL6 TETNG
23	152.5	10.7	52	2	Q4S205 TETNG
24	138	9.7	29	2	Q4WSD7 HUMAN
25	110.5	7.7	2287	2	Q8I520 PLAF7
26	110	7.7	1244	2	Q51RT1 MAGGR
27	109	7.6	392	2	Q9I8G8 CHEMY
28	109	7.6	875	2	Q5FWN0 XENLA
29	108	7.6	800	2	Q5AH61 CANAL
30	108	7.6	800	2	Q5AIP1 CANAL
31	107.5	7.5	515	2	Q4H3L1 CIOIN

32	106.5	7.5	805	2	Q5SMF2 CRYNE
33	106	7.4	795	2	Q6EUQ1 ORYSA
34	105.5	7.4	805	2	Q5K8C2 CRYNE
35	105.5	7.4	1083	2	Q12075 PNECA
36	105.5	7.4	3140	2	Q52V19 POTV
37	104.5	7.3	1679	2	Q26607 SCHMA
38	104.5	7.3	1791	2	Q9U6D4 PLABR
39	104	7.3	1787	2	Q25645 PLABR
40	103.5	7.3	384	2	Q8V918 POTV
41	103	7.2	749	2	Q72SP6 LEPIC
42	103	7.2	749	2	Q8F2V5 LEPIN
43	103	7.2	1279	2	Q4S711 TETNG
44	102.5	7.2	751	2	Q5E9H4 BOVIN
45	102.5	7.2	1829	2	Q7XE96 ORYSA

ALIGNMENTS

RESULT 1

ID	Q8IUW5 HUMAN	PRELIMINARY;	PRT;	271 AA.
AC	Q8IUW5			
DT	01-MAR-2003	(Tremblrel. 23, Created)		
DT	01-MAR-2003	(Tremblrel. 23, Last sequence update)		
DE	01-MAR-2003	(Tremblrel. 23, Last annotation update)		
DE	Similar to expressed sequence AA536743.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Pancreas;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,			
RA	Schurch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Pancreas;			
RA	Strausberg R.;			
RL	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC039540; AAH39540.1; -; mRNA.			
DR	Ensembl; ENSG00000181826; Homo sapiens.			
SQ	SEQUENCE 271 AA; 29340 MW; D85AAA086349EA7 CRC64;			

Query Match 100.0%; Score 1426; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 3.2e-100;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAPRALPGSAVLAFAVFGGAVSSPLVAPDNGSRSLHSRTTTPPSNDTNGHPEYIA	60
Db	1	MAPRALPGSAVLAFAVFGGAVSSPLVAPDNGSRSLHSRTTTPPSNDTNGHPEYIA	60


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QY 250 GAETVNGEVPATPVKRSRSGTE 271
Db 181 GIESVNGDVPATPVKRSRSDTE 202

RESULT 4
Q5P3A4_CHICK
ID Q5P3A4_CHICK PRELIMINARY; PRT; 288 AA.
AC Q5P3A4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN OAPNames=RCJMB04.24124;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
RT gene function analysis.";
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ851746; CAF65380.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 288 AA; 31157 MW; 07DC2D83E938C7BD CRC64;

Query Match 59.9%; Score 854.5; DB 2; Length 288;
Best Local Similarity 61.0%; Pred. No. 9.3e-57;
Matches 177; Conservative 36; Mismatches 50; Indels 27; Gaps 8;

QY 1 MAPRALPGSAVLA-----AAVFVGAVSSPLVADPNSSRTLHSR--TETTPSPSNDTGN 53
Db 1 MAPPAASGIPSIAPSLGPTAWLGN-----RSDLDGVQALASRDLPFTTTVTAGNNKP 53

QY 54 GHPEYIAYLVVPFFIMGLFGVLICLLKKGYRCTTEASQDIEERKV-EKIELNDVSNE 112
Db 54 EHLEYVAFVLVPFFIMGLILICLVKKGVRTCTTEAEVEEERKPDSEKNETAHE 113

QY 113 NSDTVGQIVHYIMKNEANADVLRKAVADNSLYDPESPVTPTSPGSPVPSFG-PLSPGGTP 171
Db 114 NSDTVGQIIVYIMKNEANADVLRKAVADSSVFEPSPSPNAPGS-PTSPGSPSPGAS 172

QY 172 GKHYC-GHLLHTVGGVVERDVCHRCRHWFIKPTNKSRESRPRRQGEVTVLSVGRFRV 230
Db 173 LGHCKGHLLHTVGGVTEKDCSRCSKRWHHIKPAHKSKEHRRSLRGLGEVTVLSVGRFRV 232

QY 231 TKVEHKSQKRSLSMSVSGAETVNGEVPATPVKRE-----RSGTE 271
Db 233 TKVEHKSRSKRSLSMSVTVGELGNDMPATPVKQEAKEAPATPVKEGTQ 282

RESULT 5
Q8R3S5_MOUSE
ID Q8R3S5_MOUSE PRELIMINARY; PRT; 143 AA.
AC Q8R3S5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE AA536743 protein (Fragment).
GN Name=AA536743;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

QY 250 GAETVNGEVPATPVKRSRSGTE 271
Db 181 GIESVNGDVPATPVKRSRSDTE 202

STRAIN=CZECH II;
TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Colling P.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
Schnerch A., Schein J.B., Jones S.J.M., Matra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024679; AAH24679.1; -; mRNA.
MG1; MG1:2140767; AA536743.
FT NON TER
SQ SEQUENCE 143 AA; 15527 MW; 59547DA0F91D5D42 CRC64;

Query Match 49.08; Score 699; DB 2; Length 143;
Best Local Similarity 90.9%; Pred. No. 2.8e-45;
Matches 130; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 129 ANADILKAMVADNSLYDPESPVTPTSPGSPVPSPLSPGTPGKHVCGHLLHTVGGVVE 188
Db 1 ANADILKAMVADNSVGDIESPVTPTSPGSPVPSPLSPGATPGKHVCGHLLHTVGGVVE 60

QY 189 RDVCHRCRHWFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHKSQKRSLSMSV 248
Db 61 RDVCHRCRHWFIKPTNKTGPRRQGEVTVLSVGRFRVTKVEHKSQKRSLSMSV 120

QY 249 SGAEVNGEVPATPVKRSRSGTE 271
Db 121 SGIESVNGDVPATPVKRSRSDTE 143

RESULT 6
Q7TON2_XENLA
ID Q7TON2_XENLA PRELIMINARY; PRT; 223 AA.
AC Q7TON2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE MGC69140 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Colling P.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Stapleton M., Soares M.B., Bernaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whitening M., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RA Klein S., Strausberg R.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC056115; AAH56115.1; -; mRNA.
SQ SEQUENCE 223 AA; 24273 MW; 5EB8CD32032367AB CRC64;

Query Match 46.9%; Score 669; DB 2; Length 223;
Best Local Similarity 65.4%; Pred. No. 8.7e-43;
Matches 142; Conservative 21; Mismatches 36; Indels 18; Gaps 9;

QY 70 MGLFGLVCHLLKKGYRCTTEAEODIEBEKV--EKIELNDSVNE-NSDVTGQIVHYIMKN 127
DB 1 MGLVGLVCHLLKKGYRCTTEAEPPVEKIVGEKIEHQESTGDTNDTVDGQIVDFIMKN 60

QY 128 EANADVLKAMVADNSL-----YDPSPVTPSTPGSP--PVSP-GPLSPGTPGKHVC-G 177
DB 61 EANADVLKAMVADNSIVGDTSVFDPSPPTPTPTGSPITDPTISPTSPAETPSKUSCRG 120

QY 178 HHLHTVGGVVERDVCHRCRKHWHFIPKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHS 237
DB 121 HHLHTVGGVAERNACTRCTNKRWHPLKSPQKHKEPRRSHQGAVTVLSVGRFRVTKVEPKS 180

QY 238 NOKERSLSMSVSGAETVNGEVPATPVK---RERSGTE 271
DB 181 --KERKRLMA-DRSEGTNGEVPATPVSVDTQRSGTD 214

RESULT 7
Q6NRQ3 XENLA
ID Q6NRQ3_XENLA PRELIMINARY; PRT; 224 AA.
AC Q6NRQ3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC83066 protein.
GN Name=MGC83066;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derje J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bernaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whitening M., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RA Klein S., Strausberg R.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC070680; AAH70680.1; -; mRNA.
SQ SEQUENCE 224 AA; 24512 MW; 516BF3010B11D9F0 CRC64;

Query Match 45.0%; Score 641.5; DB 2; Length 224;
Best Local Similarity 63.8%; Pred. No. 1.1e-40;
Matches 139; Conservative 21; Mismatches 39; Indels 19; Gaps 9;

QY 70 MGLFGLVCHLLKKGYRCTTEAEODIEBEKV--EKIELNDSVNE-NSDVTGQIVHYIMK 126
DB 1 MGLVGLVCHLLKKGYRCTTEAEPPVEKIVGEKIEHQESTGDTNDTVDGQIVDFIMKN 60

QY 127 EANADVLKAMVADNSL-----SLYDPSPVTPSTPGSP--PVSP-GPLSPGTPGKHVC- 176
DB 61 EANADVLKAMVADNSIVGDTSVFDPSPPTPTPTGSPITDPTISPTSPAETPSKUSCR 120

QY 177 GHLHTVGGVVERDVCHRCRKHWHFIPKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHK 236
DB 121 GSHLHTVGGVAERNVCSRCTNKEWHLJKSPQKHKEPRRSHQGAVTVLSVGRFRVTKVEPK 180

QY 237 SNOKERSLSMSVSGAETVNGEVPATPVK---RERSGTE 271
DB 181 S--KERKRLMA-DRTEATNGEIPVTPVRVDTQRSGTD 215

RESULT 8
Q5W7X6 BRARE
ID Q5W7X6_BRARE PRELIMINARY; PRT; 280 AA.
AC Q5W7X6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE LOC553285 protein (Fragment).
GN Name=LOC553285;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner J.S., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzey D.M., Sodergren E.J., Lu X., Gibbs R.A., Páney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; et al.
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RG NIH MCC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC088389.1; -; mRNA.
FT NON TER 1
SQ SEQUENCE 280 AA; 30423 MW; 251CCA8028435E76 CRC64;
Query Match 40.7%; Score 581; DB 2; Length 280;
Best Local Similarity 49.6%; Pred. No. 5.5e-36;
Matches 123; Conservative 43; Mismatches 62; Indels 20; Gaps 9;
QY 29 PDNGSRLTHSTETTPSPNDTNGHGPXIVAVLVPFIMGLFGVLIHLKKGKGYRC 88
DB 22 PMAGSSLSTNS---TRGGNGHSGDHPENIAFLVFFFLMGLGLVLIHLKKGKGYRC 78
QY 89 TTEAQDIE-----EKVKIELDSVNE-NSDTVGQIVHYIMKNEANADVLKAMVADN 141
DB 79 TTEABEEQLEKERRDELEKGLDNTFSGNADTVGQIVHYIMKNEANSALKAMVQD- 137
QY 142 SLVDPESPVTPTSPGSPVPGPLSPG--GTPGHVCGHLLHTVGGVV-BRDVCHRCRHK 198
DB 138 SIDSEGGVPVPTPTNTPTSPSPAAPGLPPTAAKHTC-NHLHTTGTGISHKNIHCRNCQK 196
QY 199 RWHFIKTKNSRSPRQGEVTVLSVGRFVTVKHSNQKRRSLMSVSGAETVNGEV 258
DB 197 KWLRLRSSKKLDRRSHVGEVTVLSVGRFVTVKCDPKT-ARERTLLITE----PNGSV 251
QY 259 PATPVKKE 266
DB 252 SPSFASQ 259
RESULT 9
Q4SRN7_TETNG PRELIMINARY; PRT; 281 AA.
AC Q4SRN7_TETNG
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Chromosome undetermined SCAF14506, whole genome shotgun sequence.
GN ORFNames=GSTENG00013829001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygia; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Da Silva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.; et al.
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014506; CAF96695.1; -; Genomic DNA.
SQ SEQUENCE 281 AA; 30111 MW; 7809ACCF514A0325 CRC64;
Query Match 29.6%; Score 422.5; DB 2; Length 281;
Best Local Similarity 46.5%; Pred. No. 6.2e-24;
Matches 93; Conservative 33; Mismatches 53; Indels 21; Gaps 8;
QY 41 TETTPSPNDTNG-----HPEYIAYALVPFIMGLFGVLIHLKKGKGYRCTTE--- 91
DB 5 TAVSQHNATDGKNGGGADGTPNYPVLPVFPVFLGLLGVVICHVLRKRGYRCTTSPQD 64
QY 92 -ASQDIEEERKVKIELDSVNE-NSDTVGQIVHYIMKNEANADVLKAMVADNLYDPSPV 150
DB 65 GGREANEKDEMG-EDADDSDHDTLQIVRCIMSEANSALKAMVHENSVDSDGPP 123
QY 151 TPSTPGSPVPGPLSPGPTG--KVCVGHLLHTVGGVVERDVCHRCRHKWHFI-KPTN 207
DB 124 TP-----SPPMT--PVSPDAPPGAAKHTCS-HLATVGGTGLKNTCTRCSSQKKWPLMRPSP 176
QY 208 KSRESRPRQGEVTVLSVGR 227
DB 177 RKAEQRRSAGVTVLAAGR 196
RESULT 10
TR19L_MACFA
ID TR19L_MACFA STANDARD; PRT; 430 AA.
AC QN092;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 19L precursor
DE (Receptor expressed in lymphoid tissues).
GN Name=TNFRSF19L; Synonyms=REL; ORFNames=QCE-10051;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain cortex;
RX MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.; et al.
RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
RT chromosomes.";
RL Gene 275:31-37(2001).
RN [2]
RP ERRATUM.
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K., Kusuda J.;

Gene 278:267-267(2001).

CC -1- FUNCTION: Mediates activation of NF-kappa-B (By similarity). May
 CC play a role in T-cell activation.
 CC -1- SUBUNIT: Associates with TRAF1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
 CC -1- SIMILARITY: Contains 1 TNFR-Cys repeat.

CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 CC EMBL: AB046039; BAB01621.1; -; mRNA.
 CC HSSP: Q92956; IJMA.
 CC InterPro: IPR001368; TNFR_C6.
 CC SMART; SM00208; TNFR; 1.
 CC PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
 CC PROSITE; PS00050; TNFR_NGFR_2; FALSE NEG.
 KW Glycoprotein; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 26 By similarity.
 FT CHAIN 27 430 Tumor necrosis factor receptor
 FT superfamily member 19L.
 FT TOPO_DOM 27 162 Extracellular (Potential).
 FT TRANSMEM 163 183 Potential.
 FT TOPO_DOM 184 430 Cytoplasmic (Potential).
 FT REPEAT 50 90 TNFR-Cys.
 FT CARBOHYD 149 149 N-linked (GlcNAc...) (Potential).
 FT DISULFID 51 65 By similarity.
 FT DISULFID 71 90 By similarity.
 SQ SEQUENCE 430 AA; 45851 MW; BA8DB92593E1E859 CRC64;

Query Match 21.78; Score 309; DB 1; Length 430;
 Best Local Similarity 31.08; Pred. No. 4.2e-13;
 Matches 84; Conservative 37; Mismatches 68; Indels 82; Gaps 12;

QY 44 TPSPNDTNGHPB-----YIAVALVPVFFTMGLFGLVILCHLLKKGRCYRTIEA----- 93
 Db 144 TRPENGTRAGGEETAAQAVTAIVPVFCMLGGLGILVNCNLLKRGYHCTAHEVGP 203

QY 94 -----QDIEEKVEKIELNDVNSYNSDVTGQIVHYIMKNEANADVLKAMVAD 140
 Db 204 GGGGSGINPAYRTEDV-----NEDTIGLVRLITKKNAAALEELKE 247

QY 141 NSLYDESPYTPSPGPPSPGLSPGCTPGKVC--GHLHTVGV--VERDVCHRCR 196
 Db 248 ---YHSKQLVQTS---HRPVSKLPPAPPNPV--HICPHRHLLHFTVQGLASLGPCCSRCS 299

QY 197 HKRWHTF-----KPTNKSRE--SRPRQGEVTLVSGVFRVTKVEHS 237
 Db 300 QKWPEVLLSPEAVAATTSAPSFLPNTRVPKAKAGKAGQGEITILSVGRFVRVARI----- 355

QY 238 NQKERSLMSVSGAETVN-----GEVPATP 262
 Db 356 --PEQRTGSMVSEVKTTITAGSGAGDLDPSP 384

RESULT 11
 TR19L HUMAN
 ID TR19L HUMAN STANDARD; Q96V34; Q96JUL; Q9BUK7; PRT; 430 AA.
 AC Q96924; Q96V34; Q96JUL; Q9BUK7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 19L precursor
 DE (Receptor expressed in lymphoid tissues).
 GN Name=TNFRSF19L; Synonyms=REL1;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF N-TERMINUS, AND INTERACTION
 RP WITH TRAF1.
 RC TISSUE=Lymphoma;
 RX MEDLINE=21213541; PubMed=11313261; DOI=10.1182/blood.V97.9.2702;
 RA Sica G.L., Zhu G., Tamada K., Liu D., Ni J., Chen L.;
 RT "REL1, a new member of the tumor necrosis factor receptor superfamily,
 RT is selectively expressed in hematopoietic tissues and activates
 RT transcription factor NF-kappaB.";
 RL Blood 97:2702-2707(2001).
 RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Retinoblastoma;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiya S., Konai F., Hara R., Takeuchi K., Arita M.,
 RA Inose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yosehikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Koniyama M., Tashiro H., Tanigami A., Fujiiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao H., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT VAL-332.
 RC TISSUE=Blood, Colon, and Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Heide F.,
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 121-430.
 RC TISSUE=Spleen;
 RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
 RT "The nucleotide sequence of a long cDNA clone isolated from human

RT spleen.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP PROTEIN SEQUENCE OF 26-40.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824 (2004).
CC -1- FUNCTION: Mediates activation of NF-kappa-B. May play a role in T-
CC cell activation.
CC -1- SUBUNIT: Associates with TRAF1.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Highest levels are in spleen, lymph node,
CC thymus, peripheral blood leukocytes, bone marrow and fetal liver.
CC Very low levels in skeletal muscle, testis and colon. Not detected
CC in brain, kidney and pancreas.
CC -1- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC -1- CAUTION: Ref.4 sequence differs from that shown due to several
CC frameshifts.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF319553; AAK77356.1; -; mRNA.
CC EMBL; AK027899; BAB55441.1; -; mRNA.
CC EMBL; BC001812; -; NOT ANNOTATED CDS; mRNA.
CC EMBL; BC017279; AAH17279.1; -; mRNA.
CC EMBL; BC051810; AAH51810.2; -; mRNA.
CC EMBL; AK074128; BAB84954.1; ALT_FRAME; mRNA.
CC HSP; Q92956; IJMA.
CC Ensembl; ENSG0000054967; Homo sapiens.
CC HGNC; HGNC:13764; TNFRSF19L.
CC H-InvDB; HIX0009918; -.
CC InterPro; IPR001368; TNFR_c6.
CC SMART; SM00208; TNFR; 1.
CC PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
CC PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
KW Direct protein sequencing; Glycoprotein; Polymorphism; Receptor;
KW Signal; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 430
FT FT
FT FT
FT TOPO_DOM 26 162 Tumor necrosis factor receptor
FT TRANSDOM 163 183 superfamily member 19L.
FT TOPO_DOM 184 430 Extracellular (Potential).
FT REPEAT 50 90 Potential.
FT CARBOHYD 149 149 Cytoplasmic (Potential).
FT DISULFID 51 65 TNFR-Cys.
FT DISULFID 71 90 N-linked (GlcNAc. .) (Potential).
FT VARIANT 332 332 By similarity.
FT FT A -> V (in dGSP:12362779).
FT FT /FTID=VAR_022614.
FT FT
FT CONFLICT 122 122 D -> S (in Ref. 4).
FT CONFLICT 187 187 K -> E (in Ref. 2).
FT CONFLICT 273 273 H -> R (in Ref. 2).
SQ SEQUENCE 430 AA; 46092 MW; 4A5AB9AE32D36101 CRC64;
Query Match 21.5%; Score 307; DB 1; Length 430;
Best Local Similarity 31.0%; Pred. No. 6e-15;
Matches 84; Conservative 36; Mismatches 69; Indels 82; Gaps 12;
QY 44 TPSPSNDTGNHPE-----YIAVALVFPFMGLFGVLI CHLLKKGYRCTTEAF----- 93
DB 144 TRFGNGTRAGPEETAQAQVAIVAFVFCMLGGLGLVLCNLLKRGYHCTAKHEVGPGP 203
QY 94 -----QDIEEKVEKIELNDVNSNEDTGVGVHYIMKYEANADVLKAMVAD 140
DB 204 GGGSGINPAYRTD-----ANEDTIGLVRLITEKKNAAALEULKE 247
QY 141 NSLYDPSPVTPPTGSPFPVSPGSLSPGPGTGGKHC--GHHLTVGGV--VERDVCHRCR 196

Db 248 ----YHSKQLVQTS---HRPVSKLPPAPPNVF---HICPHRHLLHTVQGLASLSGCCSRCS 299
QY 197 HKWHFI-----KPTNKSRE-SRPRQGEVTLVSGFRFVTKVSHKS 237
Db 300 QKMWPEVLLSPPEAAATTPVPVSLLPNPTRPVKAGAKAGROGEITILSVGRFVARI----- 355
QY 238 NQKERSLSMSVSGAETVN-----GEVPATP 262
Db 356 --PEQRTSSMVSEVKITTEAGPSWGLDLPSP 384
RESULT 12
TRI9L_MOUSE
ID TRI9L_MOUSE STANDARD; PRT; 436 AA.
AC Q8BX43; Q8BV0;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 19L precursor.
GN Name=TNFRsf19L;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J and NOD; TISSUE=Cerebellum, and Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Sono H., Kondo S.,
RA Nikaiki Y., Osato N., Saito K., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer J.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Negashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Varado R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
CC -1- FUNCTION: Mediates activation of NF-kappa-B. May play a role in T-
CC cell activation (By similarity).
CC -1- SUBUNIT: Associates with TRAF1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -1- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AK049073; BAC33534.1; -; mRNA.
CC EMBL; AK088621; BAC40459.1; -; mRNA.
DR

```
DR HSP; P19438; 1EXT.
DR Ensembl; ENSMUSG0000008318; Mus musculus.
DR MGI; MGI:2443373; Tnfref19l.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001368; TNFR_c6.
DR SMART; SM00208; TNFR; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR PROSITE; PS50050; TNFR_NGFR_2; FALSE NEG.
KW Glycoprotein; Receptor; Signal; Transmembrane.
FT SIGNAL 1 31
FT CHAIN 32 436
FT   Tumor necrosis factor receptor
FT   superfamily member 19L.
FT   Extracellular (Potential).
FT   Potential.
FT   Cytoplasmic (Potential).
FT   TNFR-Cys.
FT CARBOHYD 156 156 N-linked (GlcNAc. .) (Potential).
FT DISULFID 58 72 By similarity.
FT DISULFID 78 97 By similarity.
FT CONFLICT 39 39 G > C (in Ref. 1; BAC40459).
SQ SEQUENCE 436 AA; 46472 MW; 1F96C5E021945DF9 CRC64;

Query Match 20.7%; Score 295.5; DB 1; Length 436;
Best Local Similarity 30.6%; Pred. No. 4.5e-14;
Matches 82; Conservative 36; Mismatches 89; Indels 61; Gaps 12;

QY 31 NGSRLHSRTETTPSPNDTNGHPE-----YIAYALVVPVFMGLFGVLICHLLKKG 85
DB 148 NGEPR-----QFGNGTRAGGPETAQAQVAIVFVFLGMLGLILVCLNLLKRG 197
QY 86 YRCTTEARQDIEB---EKVEKIELNDNVNENSDTGVQIVHYIMKNEANA----DVLKAM 137
DB 198 YHCTAQKEVPSGGGGSGINPAYREDANE--DTIGVLRLTEKKNAAALBELKEY 255
QY 138 VADNSLYDPSPVTPSPGPPVSPGLSPGTPGKHVC--GHHLHTVGGV--VERDVCH 193
DB 256 HSKQLVQTSRHPVRLLPASPSI-----PHICPHHLHTVQGLASLSGPGCS 303
QY 194 RCHKEWHFI-----KPT-----NKSR-----ESRPRROGEVTVLSVGRFRVTKVE 234
DB 304 RCSQK-WPEVLLSFEAAAAATPAPTLLPTASRAPKASAKPGRQGEITILSVGRFRVARIP 362
QY 235 HKSQKERSLSMSVSGAETVNGEVPATP 262
DB 363 EQRTSLLSEVKITTEAGPSEGDLPSF 390

RESULT 13
Q8CFT0_MOUSE PRELIMINARY; PRT; 294 AA.
AC Q8CFT0_MOUSE
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RIKEN cDNA 4631403P03.
GN Name=4631403P03Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038500; AAH38500.1; -; mRNA.
DR Ensembl; ENSMUSG00000044024; Mus musculus.
DR MGI; MGI:1918044; 4631403P03Rik.
SQ SEQUENCE 294 AA; 31456 MW; 8A5DEDE20243EAF6 CRC64;

Query Match 20.3%; Score 289; DB 2; Length 294;
Best Local Similarity 38.4%; Pred. No. 9.1e-14;
Matches 86; Conservative 28; Mismatches 82; Indels 28; Gaps 9;

QY 55 HPYIAYALVVPVFMGLFGVLICHLLKKGYRCTTEAEQDIEEKVEKIELNDNVNENS 114
DB 13 HGLYMLFLVLVFLVFLGLVFMFCHLVKKGYRCTSRGSEPDQAQLQPPE-DDDVNE-- 69
QY 115 DTGGQIVHYIMKNEANADVLKAMVADNSLYDPSPVTPSPGPPVSPGLSPGTPGKH 174
DB 70 DTVERIVRLCIQNEANAEALKEMLGDS---EGEGTVQLSS-----VDATSSLOQGAESH 121
QY 175 VCGHLHTVGGVVERDVCHRCRWHFIKP-TNKSRESRPRQGEVTVLSVGRFRVTKV 233
DB 122 -----HTVHLSAACPICHSRSKRPPLVQRSGKEGSRP-RPGETTVSVGRFRVTHI 174
QY 234 -----EHKSQKERSLSMSVSGAETVNGEVPATPVKERSGT 270
DB 175 EKRYGLHHRDGSPTDRSMGSGGQBP--GGSQAAGGQPRGTGT 216

RESULT 14
Q8BRJ3_MOUSE PRELIMINARY; PRT; 303 AA.
AC Q8BRJ3_MOUSE
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
DE library, clone:A830089I08 product:hypothetical protein, full insert
DE sequence.
GN Name=4631403P03Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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Db	70	--NEDTVRIVKCI IQEANAELKQMLGDT--EGEVPIVPSLCLHRESQDAGPP----	120
Qy	164	PLSPGGTPGKHVCGHLLHTVGGVVERDVCHRCRHKRWHPFKPTNKSRESRPR-RQGEVTV	222
Db	121	-----HH-HTVHLGSTQAPCIHCTRKRSLLHRMGRSKEGKGSHPGEVTV	165
Qy	223	LSVGRFRVTKEHKSQKERRSLMSVSGAETVNGEVPAT-----PVKRERS	268
Db	166	FSVGRFRVTHIGKH-----SIQSGDSQOE-PASSDKNHEBQFVWRKSS	209

Search completed: February 23, 2006, 12:07:49
Job time : 234 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 12:04:08 ; Search time 40 Seconds
(without alignments)
651.869 Million cell updates/sec

Title: US-10-620-562-2

Perfect score: 1426

Sequence: 1 MAPALPGSAVLAAAVFG.....ETVNGEVPATPVKRSRGTE 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105.5	7.4	1083	2 JC2300	cell surface glyco
2	104.5	7.3	1679	2 T30271	surface protein -
3	98.5	6.9	3140	2 S47508	genome polyprotein
4	97.5	6.8	1541	2 AG2474	heterocyst glycoli
5	97	6.8	514	2 A31643	cell adhesion 80K
6	96.5	6.8	345	2 S55377	urPAB protein prec
7	96.5	6.8	942	2 JC7316	testicular zinc fi
8	95.5	6.7	634	2 T00359	hypothetical prote
9	94	6.6	682	2 A42121	transcription fact
10	94	6.6	1062	2 T46444	hypothetical prote
11	93.5	6.6	349	2 T25236	hypothetical prote
12	93.5	6.6	452	2 S47633	RXR protein - Afri
13	93.5	6.6	3084	1 MMMSA	laminin alpha-1 ch
14	92.5	6.5	3141	1 GNVSPD	genome polyprotein
15	92	6.5	120	2 T29774	hypothetical prote
16	91.5	6.4	513	2 AB2504	hypothetical prote
17	91.5	6.4	707	2 A46691	E-box-binding prot
18	91.5	6.4	843	2 S33442	EF protein - Strept
19	91.5	6.4	1199	2 T13946	probable adaptor-r
20	91.5	6.4	1822	2 S33441	EF protein - Strept
21	91	6.4	514	2 A44100	cell adhesion mole
22	91	6.4	706	2 S19958	basic helix-loop-h
23	89.5	6.3	467	2 A43781	retinoid-X-recepto
24	89.5	6.3	612	2 T02414	probable protein k
25	89.5	6.3	2061	2 T13751	transcription fact
26	89	6.2	512	2 T16157	hypothetical prote
27	89	6.2	605	2 S48940	hypothetical prote
28	89	6.2	2364	2 A56577	microtubule-associ
29	89	6.2	3125	1 GNVSPD	genome polyprotein

30	88.5	6.2	563	2 T49681	MCX1 related prote
31	88	6.2	355	2 H90429	membrane conserved
32	88	6.2	441	2 I50515	retinoid X recepto
33	88	6.2	909	2 AG3314	exonuclease ABC c
34	88	6.2	3869	2 A48205	All-1 protein +STE
35	88	6.2	5107	2 T29144	partial CDS - Caen
36	87.5	6.1	940	2 S19702	fibronectin-bindin
37	87.5	6.1	1420	2 B57062	SRB9 protein - yea
38	87	6.1	890	2 E81576	translation initia
39	87	6.1	890	2 E86530	initiation factor-
40	87	6.1	890	2 F72093	translation initia
41	86.5	6.1	232	2 B96803	hypothetical prote
42	86.5	6.1	879	2 S23006	shed acute-phase a
43	86.5	6.1	916	2 I48921	DNA ligase (ATP) (
44	86	6.0	553	2 B55514	dihydrolipoamide S
45	86	6.0	759	2 T16368	hypothetical prote

ALIGNMENTS

RESULT 1

JC2300

cell surface glycoprotein MSG100 - Pneumocystis carinii

C:Species: Pneumocystis carinii

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: JC2300

R:Wada, M.; Nakamura, Y.

DNA Res. 1, 163-168, 1994

A:Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis

A:Reference number: JC2299; MUID:96051989; PMID:8535973

A:Accession: JC2300

A:Molecule type: DNA

A:Residues: 1-1083 <WAD>

A:Cross-references: UNIPROT:Q12075; UNIPARC:UPI000006BAE6; GB:D31909; GB:D17441; NID:955

C:Genetics:

A:Gene: MSG100

C:Superfamily: Pneumocystis carinii major surface glycoprotein MSG100

C:Keywords: glycoprotein

Query Match 7.4%; Score 105.5; DB 2; Length 1083;
Best Local Similarity 25.3%; Pred. No. 2.5;
Matches 37; Conservative 22; Mismatches 50; Indels 37; Gaps 5;

Qy	71	GLFGVLICLLKKGVRC	TT-----EAEQDIEEKVEKIELNDSVNSSTVQIVHYI	124
Db	734	GTKGTVCKELVKKKRC	PTLKDGLNKADELTKKKEYDELKKAABESTEKALLLSKS	793
Qy	125	MK-----NEANADVLKAMVADNSLYDPESPVTPTSPGSP	-----PVSPG-----	163
Db	794	GKVAMPQDSNGSGPV	PAGSGSGSPSPAPVPPPGSPQNGTPTGTPGGTGASGGTPG	853
Qy	164	-PLSPGGTPEGKHVCG	HHLHTVGGVVE	188
Db	854	TPGTPGGAGP-----	TPGGMMK	870

RESULT 2

T30271

surface protein - fluke (Schistosoma mansoni)

C:Species: Schistosoma mansoni

C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

C:Accession: T30271

R:Hall, T.M.; Joseph, G.T.; Strand, M.

Exp. Parasitol. 80, 242-249, 1995

A:Title: Schistosoma mansoni: molecular cloning and sequencing of the 200-kDa chemothera

A:Reference number: Z2800; MUID:95203407; PMID:7534724

A:Accession: T30271

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1679 <HAL>

A:Cross-references: UNIPROT:Q25607; UNIPARC:UPI0000074F18; EMBL:M99494; NID:9501208; PID

Query Match		7.3%;	Score 104.5;	DB 2;	Length 1679;		
Best Local Similarity		22.8%;	Pred. No. 5.2;				
Matches		51;	Conservative	31;	Mismatches 73; Indels 69; Gaps 10;		
QY	79 HLLKKGYRCTTE-----	AEQDIEBEKVEKIELNDS--VNENSDTV--	117				
	:	: :	:				
Db	634 HLLDIRAYHQLDENNVDSQLKILTQRSGCCSPSESEDEVVAVSLQKDGQCSTDNNDIITC	693					
QY	118 -----GQIVHYIMKNEANADVLAADVANSILYDPESPVTPTGSPVSPGLSPGCTPG	172					
	:	:	:				
Db	694 TRTIHQIIQFKLNNPSTSDYKLYMKSDGVEDN-----VESTSIDLVTSGL--GETVK	747					
QY	173 KHVCG-----HH-----	LHTGGVVVERDVCHRCRKHWHFIKP-----TN	207				
	: :	: :	:				
Db	748 EDIKGAGLSLTVGEIHNNHETQETELDVAVHIAASKVISDNIACRPTVYLLLEFIEPNLETL	807					
QY	208 KSRESR-----PRQGEVTV-----LSVGRFRVTKVEHKSQ	239					
	:	:	:				
Db	808 KSRVSSKQTMFRINKLPSNKEINLKMQLSIGSVDPDTQSEATTNQ	851					
RESULT 3							
S47508							
genome polyprotein - plum pox virus (isolate PVV-SC)							
N;Contains: coat protein; protein 6K1; protein 6K2; protein CI; protein HCpro; protein N							
C;Species: plum pox virus, PPV							
A;Variety: isolate PVV-SC							
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004							
A;Accession: S47508							
R;Maiss, E.; Deborre, G.; Jellmann, W.; Casper, R.							
Submitted to the EMBL Data Library, August 1994							
A;Description: Complete nucleotide sequence of a plum pox potyvirus isolate (PVV-SC) der							
A;Reference number: S47508							
A;Accession: S47508							
A;Molecule type: genomic RNA							
A;Residues: 1-3140 <NAI>							
A;Cross-references: UNIPROT:Q84925; UNIPARC:UPI00000F3F01; EMBL:X81083; NID:G531731; PID							
A;Experimental source: isolate PVV-SC							
C;Superfamily: tobacco etch virus genome polyprotein							
C;Keywords: ATP; coat protein; genome-linked protein; nucleotide binding; P-loop; phosph							
F;1-308/Product: protein P1 #status predicted <P1>							
F;309-766/Product: protein HCpro #status predicted <HCP>							
F;767-1116/Product: protein P3 #status predicted <P3>							
F;1117-1168/Product: protein 6K1 #status predicted <6K1>							
F;1169-1803/Product: protein CI #status predicted <CI>							
F;1253-1260/Region: nucleotide-binding motif A (P-loop)							
F;1338-1343/Region: nucleotide-binding motif B							
F;1342-1345/Region: DEXH motif							
F;1804-1856/Product: protein 6K2 #status predicted <6K2>							
F;1857-2292/Product: protein N1a #status predicted <N1a>							
F;1857-2049/Product: VPg protein #status predicted <VPg>							
F;2293-2810/Product: protein N1b #status predicted <N1b>							
F;2811-3140/Product: coat protein #status predicted <COA>							
F;1919/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted							
Query Match		6.9%;	Score 98.5;	DB 2;	Length 3140;		
Best Local Similarity		24.7%;	Pred. No. 35;				
Matches		45;	Conservative	27;	Mismatches 85; Indels 25; Gaps 6;		
QY	83 KKGRCYCTTEAQDIEEBE-KVEKIELNDSVNENSDTVGQIVHYIMKNEANA----	DVLKAMV	138				
	:	:	:				
Db	2774 KLYTDTAESEIERLYLKAFYDDINDD-GESNVVVHVQVAEREDEBEVNAGKSNVVTAPA	2832					
QY	139 ADNSLYDP-----ESPVTPTPGSPVSPGLSPGCTPGKHVCGHLLHTVGGVVERDVCH	193					
	: :	:	:				
Db	2833 ATPILQPLVIOQAPRTTASMLNPIFTPATTPATKFPVQSQVSPQLQTFGTGYGNEDA--	2890					
QY	194 RCRKHWHFIKPTNKSRESRPRRGQEVTVLSVGRFRVTKVEHKSQKERSLSMVSQAET	253					
	:	:	:				
Db	2891 -----SPGNSNALVNTSRDRVDAGSTGTFVPLKAMTMS-----KLSLPKVKGKAI	2937					
QY	254 VN 255	:					

Db

2938 MN 2939

RESULT 4

AG2474

heterocyst glycolipid synthase [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AG2474

R;Kakano, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AG2474

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1541 <KUR>

A;Cross-references: UNIPROT:Q8YLE7; UNIPARC:UPI00000CEES2; GB:BA000019; PIDN:BA077050.1;

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: hglE

Query Match 6.8%; Score 97.5; DB 2; Length 1541;

Best Local Similarity 21.3%; Pred. No. 17;

Matches 45; Conservative 30; Mismatches 73; Indels 63; Gaps 8;

QY 1 MAPRA--LPGSAVLA--AAVFGG-----AVSSPLVAPDNGSSRTLHSRTLTSTTTPSPSNDTG 52

Db 1248 LAPTAQIQSEPVVAATASVSVSTIEPEPVIEADVAAP-----VAVQVVEFTSAP----- 1296

QY 53 NGHPEVIAALVVPFIMGILFGLVILCHLLKKGY-----RCTTEAEQDIEEEKVEKIELN 107

Db 1297 -----APVAAPADIVADLDKNLTAIISDKTGPVEMLEMDMEADLGIDSIRKVEIL 1349

QY 108 DSYNE-----NSDFTVGQIVHYIMKNEA-----NADVLKAMVAD 140

Db 1350 GGLQEVYVPLPKNLELAEKRTIGQIVLYLKANTAIQSQVGTAIQAQAAPAPVVT 1409

QY 141 NSLYDPSPVPTPGSPVSPGLSPGCTPG 171

Db 1410 ASIAAPEPVVAPT-----PIAPEPVVAPATP 1435

RESULT 5

A31643

cell adhesion 80K glycoprotein precursor - slime mold (Dictyostelium discoideum)

N;Alternate names: cell adhesion molecule csa; cell surface glycoprotein, 80K

C;Species: Dictyostelium discoideum

A;Variety: strain AX-2

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C;Accession: S22066; A31643; A26310; A23951; A33463; S01473

R;Desbarats, L.; Lam, T.Y.; Wong, L.M.; Siu, C.H.

submitted to the EMBL Data Library, June 1992

A;Description: Identification of a unique camp-responsive element in the gene encoding t

A;Reference number: S22066

A;Accession: S22066

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-514 <DES>

A;Cross-references: UNIPROT:P08796; UNIPARC:UPI00001284F3; EMBL:X66483; NID:g7289; PIDN:G

R;Kamboj, R.K.; Wong, L.M.; Lam, T.Y.; Siu, C.H.

J. Cell Biol. 107, 1835-1843, 1988

A;Title: Mapping of a cell-binding domain in the cell adhesion molecule gp80 of Dictyoste

A;Reference number: A31643; MUID:89034443; PMID:3182938

A;Accession: A31643

A;Molecule type: mRNA

A;Residues: 1-514 <RAM>

A;Cross-references: UNIPARC:UPI00001284F3; GB:M36545; NID:g167803; PIDN:AAA33212.1; PID:G

R;Noegel, A.; Gerisch, G.; Stadler, J.; Westphal, M.

EMBO J. 5, 1473-1476, 1986

A;Title: Complete sequence and transcript regulation of a cell adhesion protein from ags;

A;Reference number: A26310
A;Accession: A26310
A;Molecule type: mRNA
A;Residues: 1-215,'G',217-514 <NOE>
A;Cross-references: UNIPARC:UPI000016B99B; EMBL:X04004; NID:57246; PIDN:CAA27634.1; PID:
R;Wong, L.M.; Siu, C.H.
Proc. Natl. Acad. Sci. U.S.A. 83, 4248-4252, 1986
A;Title: Cloning of cDNA for the contact site A glycoprotein of Dictyostelium discoideum
A;Reference number: A23951
A;Accession: A23951
A;Molecule type: mRNA
A;Residues: 20-49 <WON>
A;Cross-references: UNIPARC:UPI0000000031; GB:M13546; NID:617699; PIDN:AAA33181.1; PID:
R;Kamboj, R.K.; Gariepy, J.; Siu, C.H.
Cell 59, 615-625, 1989
A;Title: Identification of an octapeptide involved in homophilic interaction of the cell
A;Reference number: A33463; MUID:90058644; PMID:2582489
A;Accession: A33463
A;Molecule type: protein
A;Residues: 132-139 <KA2>
A;Cross-references: UNIPARC:UPI000017B17A
R;Stadler, J.; Bordier, C.; Lottspeich, F.; Henschen, A.; Gerisch, G.
Hoppe-Seyler's Z. Physiol. Chem. 363, 771-776, 1982
A;Title: Improved purification and N-terminal amino acid sequence determination of the c
A;Reference number: S01473; MUID:83005404; PMID:7118072
A;Accession: S01473
A;Molecule type: protein
A;Residues: 20-37,'X',39-41,'X',43-46 <STA>
A;Cross-references: UNIPARC:UPI000017B17B
R;Stadler, J.; Keenan, T.W.; Bauer, G.; Gerisch, G.
EMBO J. 8, 371-377, 1989
A;Title: The contact site A glycoprotein of Dictyostelium discoideum carries a phosphol
A;Reference number: A56857; MUID:89251561; PMID:2721485
A;Contents: annotation; detection of glycosphingolipidinositol anchor
A;Note: no phosphoserine was detected but phosphoinositol and ceramide were
A;Note: the N-linked carbohydrates are sulfated type 1 oligosaccharides
C;Comment: This protein is involved in the formation of intercellular contacts upon aggr
A;Gene: csa
C;Keywords: blocked carboxyl end; cell adhesion; glycoprotein; lipoprotein; membrane pro
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-514/Product: cell adhesion 80K glycoprotein #status predicted <MAT>
F;132-139/Region: cell adhesion #status predicted
F;460-479/Region: 10-residue repeats
F;493-514/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;128,137,207,294,399/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;492/Modified site: GSI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match 6.8%; Score 97; DB 2; Length 514;
Best Local Similarity 19.6%; Pred. No. 4.8;
Matches 57; Conservative 50; Mismatches 116; Indels 68; Gaps 13;
Qy 16 VFVGGAVSSPLVAPDNGSSRTLHRTTTPSPN-----DTGNCHPEYIAYAL 63
Db 50 VTIGGQTCDPVIVANTASLQCFQF-AQLAPGNSFDVIVKGVGVPSTGGNGLFKYTPPTL 108
Qy 64 VPVFIMGLFG-VLICHLLKKGYRCTTEAEQDIEEKVEKIELDSVNE-----NSDTV 117
Db 109 STIFPNNGRIGMILVDGFSNISGY-----KLVNDSINAMLSVTADSV 152
Qy 118 GQIVHYIMKNEANADVL-----KAMVADNSLYDPSVPTTPSGSPVSPGGLSP 167
Db 153 SPTIYFLVPNTIAGLLNLELIQPFGSTIVTSKVSFSP--TITSITFLAFDLTFTVTV 210
Qy 168 GG-----TPGRHVCGHLLHTVGGVVERDVCHRCRKHWHFIKPTWKSRESRPRQGEVTVL 223
Db 211 TGRKYFVTASVTMGSHIYT--GLTVQDDGTNC-----HVIPTTRSVYES-----SNTITAK 259
Qy 224 SVGRFRVTYKVEHKNQKE---RRSLMSVSGAETVNGVGPATPVKRSRSGTE 271
Db 260 ASTGDVMIYLDNQGNQDQPTFTYNPPTITSTKQVNDV---EISTTWTGID 307

RESULT 6

S55377
urPAB protein precursor - Peptostreptococcus magnus
C;Species: Peptostreptococcus magnus
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
A;Accession: S55377
R;de Chateau, M.; Bjoerck, L.
submitted to the EMBL Data Library, April 1995
A;Description: Protein urPAB.
A;Reference number: S55377
A;Accession: S55377
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <DEC>
A;Cross-references: UNIPROT:Q51932; UNIPARC:UPI000000A8E7E; EMBL:Z48975; NID:g854370; PID:
Query Match 6.8%; Score 96.5; DB 2; Length 345;
Best Local Similarity 20.3%; Pred. No. 3.2; Mismatches 64; Indels 103; Gaps 7;
Matches 47; Conservative 17;
Qy 97 EEKVEKIELDSVNSNSDTVGQIVHYIMKNEANADVLKAMVADNSLYDP----- 146
Db 121 EEKAKKEAKEDVSDSWYDOSKHPPFAVTKEEAEQAQAKAL--ENELLNPGHINNSYKVS 178
Qy 147 -----ESPVTPTSPGSPVSPGLSP----- 167
Db 179 QKYDGNWEYVLSPLNAETPETPKPKSPDVTNPSTPEVEBEKOPVLPSPRLDNHYFMNG 238
Qy 168 -----GGTPGKHVCGHLLHTVGGVVERDVCHRCRKHWHFIKPTWKSRESRPRQGEV 220
Db 239 DSSTSDEGKTPGKEE-----XP-----GKEEKPGE--- 264
Qy 221 TVLSVGRFRVTYKVEHKNQKERSLMSVSGAETVNGVGPATPVKRSRSGTE 271
Db 265 -----EKPEQKPKKEKPKKEKPKPAN-PAKPAKEEKEKD 304

RESULT 7

JC7316
testicular zinc finger protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 09-Jul-2004
A;Accession: JC7316
R;Inoue, A.; Ishiji, A.; Kasagi, S.; Ishizuka, M.; Hirose, S.; Baba, T.; Hagiwara, H.
Biochem. Biophys. Res. Commun. 273, 398-403, 2000
A;Title: The transcript for a novel protein with a zinc finger motif is expressed at spe
A;Reference number: JC7316
A;Contents: testis
A;Accession: JC7316
A;Molecule type: mRNA
A;Residues: 1-942 <INO>
A;Cross-references: UNIPROT:Q9J01; UNIPARC:UPI00000285D3
C;Comment: This protein, with a zinc finger motif, functions as a transcriptional regula
in the initiation of the reduction divisions of meiosis and/or in the maintenance of mei
C;Genetics:
A;Gene: tzf
C;Keywords: meiosis; spermatogenesis; testis; transcription regulation; zinc finger

Query Match 6.8%; Score 96.5; DB 2; Length 942;
Best Local Similarity 21.4%; Pred. No. 11;
Matches 75; Conservative 39; Mismatches 134; Indels 103; Gaps 13;
Qy 5 ALPGSAVLAFAVFGGAVSSPLVAPDNGSSRTLHRTTTPSPS-----NDTNGH 55
Db 172 SIPLAGLVLTSPFGVSLQRPPEVPMMPKKSILKKRIEADMKPSLQLESFSSGASSGDH 231
Qy 56 PEYIAIVPVPFIMGLFGVLICHLLKKGYRCTTEAEQDIEEKVEKIE---LNDVSNE 112
Db 232 PLYSEHSPLSLGAIARF-----TSEIENKG---TTVEADLKPEQSNLYQWGLREIPKD 283
Qy 113 NSDTVGQIVHYIMKNEANADVLK-----AMVAD----- 140
Db 284 NSBKFDNFLGKRLDLKAEGLSEQDTNLLPHERASQDGSFGRILSMLADPTTITQEKRR 343

141 -----NSLYDPSPVT-----PSTPGSPVPSPGLSPGG 169
Db 344 RSPDIEDBKLYGDEEDIKSPKSLSDPESAGTRQKANSPLSTPAVKLESLEE-S 402
Qy 170 TPGKHVCGHHLHTVG-----GVVERDVCHRCRHKRWHFIKPTNKSRESRPRQGEVTVLSVG 226
Db 403 NPEYAKIHNLTKTIGLDIGVAEIGKLAARTQERLHGKKPS--SRPSADRLSADRHLSGD 460
Qy 227 RF-----RVTKEH-----KSNQKERSLSMSVSGAETNGEV-----PATPV 263
Db 461 RHFSADRCSSEVHSFTADWRSSDPHRPRESRTHSNTSQSPESHPPASPV 511
RESULT 8
T00359
hypothetical protein KIAA0680 - human
C/Species: Homo sapiens (man)
C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C/Accession: T00359
R:Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res. 5, 169-176, 1998
A/Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A/Reference number: Z14142; MUID:98403880; PMID:9734811
A/Accession: T00359
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-634 <ISH>
A/Cross-references: UNIPROT:O75167; UNIPARC:UPI000006E0AA; EMBL:AB014580; NID:g3327173;
A/Experimental source: brain; clone HK02746
C/Genetics:
A/Note: KIAA0680
Query Match 6.7%; Score 95.5; DB 2; Length 634;
Best Local Similarity 19.5%; Pred. No. 8.2;
Matches 52; Conservative 24; Mismatches 79; Indels 111; Gaps 10;
Qy 50 DTGNGPEYAYALVPVFFIMGLFGVLICHLKKKGYRCTTEAQDIEEEKVEKIEL-ND 108
Db 96 ENNGH-----MPL-----GEESTRENNVAKSEENG 123
Qy 109 SVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPSPVTPSTPGSPVPSP----- 162
Db 124 SVSEKTPPL-----BEQAEDEK-----ENTENHSETPAAPALPPSAPPKPSKPKP 169
Qy 163 --GPLSPGG-----TPGKHV-----CGHHLHT 182
Db 170 KGSFVPKPGATAGASHKGDSEVPPIKNTKAPGKQAPVPPPKPASRNTTREAAGSHSKKT 229
Qy 183 VGVVERDVCHRCRHKRWHFIKPTNKSRESRPRQGEVTVLSVGRFRTVKEHKSQKER 242
Db 230 TGSKAS-----ASPSTSTSRKPKASKEVTSKAGTVGTTGKGRKTDKQPI 275
Qy 243 RSLMS-----VSGAETVNGEVPATPVK 264
Db 276 TSHLSSDTTTSGLKGEPAETRV 301
RESULT 9
A42121
transcription factor HTF4 - human
N/Alternate names: helix-loop-helix protein (HEB)
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A42121; B56611; S34423; S34424
R:Hu, J.S.; Olson, E.N.; Kingston, R.E.
Mol. Cell. Biol. 12, 1031-1042, 1992
A/Title: HEB, a helix-loop-helix protein related to E2A and Irf2 that can modulate the
A/Reference number: A42121; MUID:92186835; PMID:1312219
A/Accession: A42121
A/Molecule type: mRNA
A/Residues: 1-682 <HU1>
A/Cross-references: UNIPROT:Q99081; UNIPARC:UPI000003B45E; GB:M80627; NID:g183929; PIDN:

A/Note: sequence extracted from NCBI backbone (NCBIN:88251, NCBIIP:88254)
R:Zhang, Y.; Bina, M.
DNA Seq. 2, 397-403, 1992
A/Title: The nucleotide sequence of the human transcription factor HTF4a cDNA.
A/Reference number: A56611; MUID:93076001; PMID:1446075
A/Accession: B56611
A/Molecule type: mRNA
A/Residues: 1-682 <ZHA>
A/Cross-references: UNIPARC:UPI000003B45E; GB:M83233; NID:g2243159; PIDN:AAB62389.1; PID
A/Note: sequence extracted from NCBI backbone (NCBIN:118868, NCBIIP:118873)
R:Zhang, Y.; Babin, J.; Feidhaus, A.L.; Singh, H.; Sharp, P.A.; Bina, M.
Nucleic Acids Res. 19, 4555, 1991
A/Title: HTF4: a new human helix-loop-helix protein.
A/Reference number: S34423; MUID:91360364; PMID:1886779
A/Accession: S34423
A/Molecule type: mRNA
A/Residues: 570-655 <ZH2>
A/Cross-references: UNIPARC:UPI0000176417; EMBL:M65209
C/Genetics:
A/Gene: GDB:TCF12
A/Cross-references: GDB:355444; OMIM:600480
A/Map position: 15q21-15q21
C/Superfamily: human transcription factor 3
C/Keywords: DNA binding; transcription factor
Query Match 6.6%; Score 94; DB 2; Length 682;
Best Local Similarity 20.6%; Pred. No. 12;
Matches 73; Conservative 38; Mismatches 109; Indels 134; Gaps 16;
Qy 3 PRALPGSVLAAAVFV--GGAVSSPLVADPNSSSRT----LHSRTETTPSPSNDTGNHG- 55
Db 212 PSFKPTMPASTFFMQDGTGTHSSDLWSSNGMSQPGFGILGTSTSHMSQSSSYGNLHS 271
Qy 56 -----PEYAYALVPVFFIMGLFGVLICHLKKKGYRCTTEAQDIEEEKVEK 103
Db 272 HDRLSYPPHSVSPDINTSLPP---MSSP-----HSGTSSSPYVAASHTPP 315
Qy 104 IEENDSV-----NENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPE--SPVT 151
Db 316 INGSDSLITGRNAAGSSQTDALG-----KALA---SIYSPDHTSSSF 356
Qy 152 PSTPGSPVPSPGLS-----PGG--TPGKHVCGHHLHTVGVVE-----RDVCHRCRH 197
Db 357 PSNPSTPVGSPSLTGTSPWPRFGGQAPSPSPSYENSLHSLQSRMEDRLDLDDAIHVLRN 416
Qy 198 KRWHFIKPTNK-----HVGVPSTSLPAGHSDIHSLLGPHSHNAPIGSLNSNYGGSSILVASSRSASVMGTHREDS 473
Db 417 ---HVGVPSTSLPAGHSDIHSLLGPHSHNAPIGSLNSNYGGSSILVASSRSASVMGTHREDS 473
Qy 214 PRQGEVTVL--SVGRFRTVKEHKSQKERSLMSVSGAETVNGEVPATPVKE 266
Db 474 VSLNGHNSVLSSTVTTTSTDLNKHKTQENYRGGLQSQSGT-----VVTTEIKTE 521
RESULT 10
T46444
hypothetical protein DKFPz434N1427.1 - human
C/Species: Homo sapiens (man)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: T46444
R:Bloecker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A/Reference number: Z23032
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1062 <AAA>
A/Cross-references: UNIPROT:Q9NSW2; UNIPARC:UPI000006FE55; EMBL:AL137701
A/Experimental source: adult testis; clone DKFPz434N1427
C/Genetics:
A/Note: DKFPz434N1427.1

A>Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in having 118-His
C:Superfamily: retinoic acid receptor alpha; erba transforming protein homology
C:Keywords: zinc finger
F:126-368/Domain: erba transforming protein homology <ERBA>

Query Match 6.6%; Score 93.5; DB 2; Length 452;
Best Local Similarity 23.0%; Pred.No.7.8;
Matches 60; Conservative 37; Mismatches 97; Indels 67; Gaps 15;

Qy 28 APDNGS-SRTL-HSRTEPTSPNDTGNHPIYIAVLV-----PVFFIMGLFGVLICHL 80
Db :
9 SPDTSLSPLGLHGFSDTPPPAPL---HPSWVGSAMTSSVNSPLGSGPFPVINC- 64
Qy 81 LKKGYRCTTBAGDIIEBEKVEIKELNDSVNENSDTVGOIVHYIMKNKANADVLLKAMVAD 140
Db :
65 VGSPIPGT----PSIGYGPVSSPOINSTNLSSG-----LHHVGSSE----- 102
Qy 141 NSLYDPESPVTPTPGSPVPSPGLSPGGT-PGKHVC-----GHH--LHTVGG---- 185
Db 103 ----DVKPPLGLWRSMQSHP-----NGSTVGSKRLCATCGDRSSOKHYGVHSCGCKGF 151
Qy 186 ---VVERPDVCHRCRHKRWHFKTPTNKNSRESRRROGEVTLVSVGRPRVTKEVHSKNOKER 242
Db :
152 FKRIRKDLTYTCRDSDKCIVDKQRNRNCOYCRYQ---KCLATGMKREAVQEERQRER 208
Qy 243 RSLMSVSGAETVNGEVPATPV 263
Db :
209 DGEABLSCA--INEEMPVEKI 227

RESULT 13
MMMSA
Laminin alpha-1 chain precursor - mouse
N:Alternate names: laminin chain A1
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 09-Jul-2004
C:Accession: A31771; A30449; S06624; A30450; S08895; S02678; S01790; A30451; S14670
R:Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.
J. Biol. Chem. 263, 16536-16544, 1988
A>Title: Laminin, a multidomain protein. The A chain has a unique globular domain and ho
A:Reference number: A31771, PMID:89034134; PMID:3182802
A:Accession: A31771
A:Molecule type: mRNA
A:Residues: 1-3084 <SAS>
A:Cross-references: UNIPROT:P19137; UNIPARC:UIP00000278CA; EMBL:J04064; NID:g309419; PID:
A:Accession: A30449
A:Molecule type: Protein
A:Residues: 183-195;570-571,'A',573-586;596-612,'X',614-617,'EMK';630-646;1217-1222,'YFP'
2486;7624-7639;72818-2843;3009-3033,'V',3035 <SA2>
A:Cross-references: UNIPARC:UIP0000173C92; UNIPARC:UIP0000173C93; UNIPARC:UIP0000173C94;
C99; UNIPARC:UIP0000173C9A; UNIPARC:UIP0000173C9B; UNIPARC:UIP0000173C9C; UNIPARC:UIP0000173C9D;
10000173CA2
R:Hartl, L.; Oberbauer, I.; Deutzmann, R.
Eur. J. Biochem. 173, 629-635, 1988
A>Title: The N terminus of laminin A chain is homologous to the B chains.
A:Reference number: S00624; MUID:88225080; PMID:3267223
A:Accession: S00624
A:Molecule type: mRNA
A:Residues: 1-208,'T',210-334 <HAR>
A:Cross-references: UNIPARC:UIP000016CS8F; EMBL:X07737; NID:g52857; PIDN:CAA30561.1; PID:
A:Accession: A30450
A:Molecule type: Protein
A:Residues: 311-335,'V',337-339;630-642,'D',644;692-734;737-748,'X',750-760,'G',762-763;
3-1389;1449-1459 <HA2>
A:Cross-references: UNIPARC:UIP0000173CA3; UNIPARC:UIP0000173CA4; UNIPARC:UIP0000173CA5;
CAA; UNIPARC:UIP0000173CAB; UNIPARC:UIP0000173CAC
A>Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-Ile
R:Mann, K.; Deutzmann, R.; Timpl, R.
Eur. J. Biochem. 178, 71-80, 1988
A>Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th
A:Reference number: S08895; MUID:89078415; PMID:2462498
A:Accession: S08895
A:Molecule type: Protein

Job time : 42 secs

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Result No.	Score	Query Match	Length	DB	ID	Description	
1	1291	100.0	1291	3	US-09-910-562-1	Sequence 1, Appli	
2	1291	100.0	1291	9	US-10-620-562-1	Sequence 1, Appli	
3	1196.6	92.7	1603	3	US-09-933-767-56	Sequence 56, Appl	
4	1196.6	92.7	1603	5	US-10-004-860-56	Sequence 56, Appl	
5	1196.6	92.7	1603	5	US-10-023-282-56	Sequence 56, Appl	
6	226.2	17.5	591	4	US-09-925-065A-84619	Sequence 84619, A	
7	115.4	8.9	694	8	US-10-363-345A-5597	Sequence 5597, Ap	
8	115.4	8.9	694	8	US-10-363-345A-5598	Sequence 5598, Ap	
9	115.4	8.9	694	9	US-10-363-483A-5597	Sequence 5597, Ap	
10	115.4	8.9	694	9	US-10-363-483A-5598	Sequence 5598, Ap	
11	104.6	8.1	694	8	US-10-363-345A-5599	Sequence 5599, Ap	
12	104.6	8.1	694	8	US-10-363-345A-5600	Sequence 5600, Ap	
13	104.6	8.1	694	9	US-10-363-483A-5599	Sequence 5599, Ap	
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17	74	5.7	2205	4	US-09-925-065A-2553	Sequence 2553, Ap	
18	74	5.7	2480	4	US-09-925-065A-720502	Sequence 720502,	
19	74	5.7	2480	4	US-09-925-065A-720503	Sequence 720503,	
20	74	5.7	2480	4	US-09-925-065A-720504	Sequence 720504,	
21	74	5.7	2480	4	US-09-925-065A-720505	Sequence 720505,	
22	73	5.7	488	3	US-09-918-995-636	Sequence 636, App	
23	72.6	5.6	582	3	US-09-910-562-3	Sequence 3, Appli	

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Qy 361 CAGAAGCAGACAGATATCGAAGAGGAAAGGTTGAAAGATAGAATTGAATGACAGTG 420
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Qy 961 AGAAGTACTTGGAGCTCCAGCTGTGTGAGCATAGGAATGATTTGACAGGGAA 1020
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Qy 1021 GTGGGAGAGCTTCTTGAACCCAGAGACTGAGGGGAGCTGAACATGATTTACTTGTCTG 1080
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RESULT 2

US-10-620-562-1

; Sequence 1, Application US/10620562

; Publication No. US20050090436A1

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; GENERAL INFORMATION:
; APPLICANT: Zeng, Z et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor receptors TR21 and TR22
; FILE REFERENCE: PF530C1
; CURRENT FILING DATE: 2003-07-17
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 09/910,562
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 60/221,143
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/220,116
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1291
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-620-562-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 661 ATGTGTGTCTATCGGTGTAGGCACAGCGGTGGCACTTTTATAAGCCCACTAAACAAGTCCA 720
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; Sequence 56, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,895
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; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
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; PRIOR APPLICATION NUMBER: 60/070,923
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PRIOR APPLICATION NUMBER: 60/085,923
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PRIOR APPLICATION NUMBER: 60/085,922
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/094,657
PRIOR FILING DATE: 1998-07-30
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SEQ ID NO 56
LENGTH: 1603
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (328)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (336)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (341)
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OTHER INFORMATION: n equals a,t,g, or c
US-09-933-767-56

Query Match 92.7%; Score 1196.6; DB 3; Length 1603;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1268; Conservative 5; Mismatches 13; Indels 9; Gaps 6;

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DB	124	CGGTCTAGCCGCTGTCTTGCTGGGAGGCGCGGTGAGTTGCGCGCTGGTCCCG	183
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DB	184	ACAATGGGAGCAGCCGACATTTGCATCCAGAACAGACGACCGCGTCCGAGCACG	243
QY	241	ATACTGGGAATGACACCAGAAATATTGCATAGCGCTTGCTCCTGTGTTCTTTATCA	300
DB	244	ATACTGGGAATGACACCAGAAATATTGCATAGCGCTTGCTCCTGTGTTCTTTATCA	303
QY	301	TGGGTCTCTTTGGCGTCTCATTTGCCACTTCG---TTAAGAAGAAAAGGCTATCGTTGA	357
DB	304	TGGGTCTCTTTGGCGTCTCATTTNGCCAMCTNGCTTNAAGAAGAAAAGGCTATCGTTGA	363
QY	358	CACACAGCAGCAGCAAGATATCGAAGG-AAAGGTTGAAAAATAGAAATGATGAC	416
DB	364	CACACAGCAGCAGCAAGATATCGAAGGAAAAGGTTGAAAAGTAGRATTGAATGAC	423
QY	417	AGTGTGAATGAAAACAGTGACACTGTTGGGCAAATCGTCCACTACATCATGAAAATGAA	476
DB	424	AGTGTGAATGAAAACAGTGACACTGTTGGGCAAATCGTCCACTACATCATGAAAATGAA	483
QY	477	GCGAATGCTGATGCTTTAAAGGCGAATGGTAGCAGATAACAGCCTGTATGATCCTGAAAGC	536

Db 484 GCGAATGCTGATGCTTTAAAGGCGAATGGTAGCAGATAACAGCCTGTATGATCCTGAAAGC 544

QY 537 CCCTGACCCCCCAGCAGACACACAGGGAGCCCGCCAGTGAGTCCCTGGGCCCTTTGTACACAGGG 596

DB 544 CCCTGACCCCCCAGCAGACACACAGGGAGCCCGCCAGTGAGTCCCTGGG-CTTTGTACACAGGG 602

QY 597 GGACCCGAGGGAAGCACGCTCTGTGGCCCATCATCTGCATACGGTGGGCGGTGTTGTGAG 656

DB 603 GGGACGCCAGGGAAGCACGCTCTGTGGCCCATCATCTGCATACGGTGGGCGGTGTTGTGAG 662

QY 657 AGGATGTGTGTCATCGGTGTAGGCACCAAGCCGTGGCAGCTTTATTAAGCCCACTAACAG 716

DB 663 AGGATGTGTGTCATCGGTGTAGGCACCAAGCCGTGGCAGCTTTATTAAGCCCACTAACAG 722

QY 717 TCCAGAGAGAGCAGACACCGCGCCCAAGCGCGGAGGTACGGTCTCTTTCTGTGGCAGATTT 776

DB 723 TCCAGAGAGAGCAGACACCGCGCCCAAGCGCGGAGGTACGGTCTCTTTCTGTGGCAGATTT 782

QY 777 AGAGTTACAAAAGTGGAGCACCAAGTCAAAACCAAGAAAGAAACCGAGAGGCTCTGATCTCTGT 836

DB 783 AGAGTTACAAAAGTGGAGCACCAAGTCAAAACCAAGAAAGAAACCGAGAGGCTCTGATCTCTGT 842

QY 837 AGTGGGCTGAAAACCGTCAATGGGAGGTGCGCGCAACACCTGTGAAGAGAAACGAGT 896

DB 843 AGTGGGCTGAAAACCGTCAATGGGAGGTGCGCGCAACACCTGTGTGAAGAGAAACGAGT 902

QY 897 GGCACAGAGTAGCAGGTAGCGGTGAGCGTGGTGGTGGTGGTGGGCGAGAGTGTGCGAGGT 956

DB 903 GGCACAGAGTAGCAGGTAGCGGTGAGCGTGGTGGTGGTGGTGGGCGAGAGTGTGCGAGGT 962

QY 957 GAGGAGAAGGTACTTTGGAGCCTCCAGSGTGTGTGGCAGCATPAGGAATGGTATTGTGACAG 1016

DB 963 GAGGAGAAGGTACTTTGGAGCCTCCAGSGTGTGTGGCAGCATPAGGAATGGTATTGTGACAG 1022

QY 1017 GGAAGTGGGAGAGCTTTCTTGACCCAGAGAGACTGAGGGGAGCTGAACATGATTACTTTG 1076

DB 1023 GGAAGTGGGAGAGCTTTCTTGACCCAGAGAGACTGAGGGGAGCTGAACATGATTACTTTG 1088

QY 1077 TCTGCCCTAGAGCTTCTGTAAAGAAAGTCAACAACTTAGTGCTCCAGGGGCTTGGCCTGT 1136

DB 1083 TCTGCCCTAGAGCTTCTGTAAAGAAAGTCAACAACTTAGTGCTCCAGGGGCTTGG-CTGT 1144

QY 1137 GTGATAATGAGGATAGAGGATTACTTTGTAGGCAATGTGGCATGTGGGGATTTGTGGCAA 1196

DB 1142 GTGATAATGAGGATAGAGGATTACTTTGTAGGCAATGTGGCATGTGGGGATTTGTGGCAA 1200

QY 1197 ACTAGAAATTCACATCACCCACCATATAGGGCTTGCAATACACAGAGGAGAGAACACCTA 1256

DB 1202 ACTAGAAATTCACATCACCCACCATATAGGGCTTGCAATACACAGAGGAGAGAACACCTA 1266

QY 1257 GTGTGCTGCATCTTCTTACGCAAAAAAAAAAAAA 1291

DB 1262 GTGTGCTGCATCTTCTTACGCAAAAAAAAAAAAA 1296

RESULT 4
US-10-004-860-56
Sequence 56, Application US/10004860
Publication No. US20030065160A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/10/004,860
CURRENT FILING DATE: 2001-12-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56
LENGTH: 1603
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

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; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (336)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (341)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (788)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-004-860-56

Query Match          92.7%; Score 1196.6; DB 5; Length 1603;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1268; Conservative 5; Mismatches 13; Indels 9; Gaps 6;

Qy 1 CCCACGGCTCGGCGCCCGGCTCCGAGCGGCTCTGCTTCCGAGCGGCGGACGGCG 60
Db 7 CCCACGGCTCGGCGCCCGGCTCCGAGCGGCTCTGCTTCCGAGCGGCGGAC--CGC 64
Qy 61 GCGCTGGGGAGGAGGCGGAGCGACCGCGATGGCTCCGCGGCGCACTCCCGGGGTCG 120
Db 65 GCGCTGGGGAGGAGGCGGAG--CGACCGCGCGATGGCTCCGCGGCGCACTCCCGGGGTCG 123
Qy 121 CCGTCTAGCGCTGCTGCTCTCTGGAGCGCGCGTGGTCCGCGCTGGTGGCTCGG 180
Db 124 CCGTCTAGCGCTGCTGCTCTGGAGCGCGCGTGGTCCGCGCTGGTGGCTCGG 183
Qy 181 ACAATGGAGCAGCGCGCACATTTGCACTCCAGACAGAGACGCCCGTCGCCAGCAACG 240
Db 184 ACAATGGAGCAGCGCGCACATTTGCACTCCAGACAGAGACGCCCGTCGCCAGCAACG 243
Qy 241 ATACTGGGAATGGACACCCAGAAATATATGTCATACGGCTTGTCCCTGTGTTCTTATCA 300
Db 244 ATACTGGGAATGGACACCCAGAAATATATGTCATACGGCTTGTCCCTGTGTTCTTATCA 303
Qy 301 TGGTCTCTTTGGCGTCTGATTTGCCACCTGC---TTAGAGAAAGGCTATCGTTGTA 357
Db 304 TGGTCTCTTTGGCGTCTGATTTNGCCAMTNGCTTNAAGAGAAAGGCTATCGTTGTA 363
Qy 358 CAACAGAGCAGACAGATATCAAGAG--AAAGGTTGAAGATAGAAATGAATGAC 416
Db 364 CAACAGAGCAGACAGATATCAAGAGAAAGGTTGAAGATAGAAATGAATGAC 423
Qy 417 AGTGTGAATGAAACAGTGACACTGTTGGGCAATCGTCCACTACATCATGAAATAATGAA 476
Db 424 AGTGTGAATGAAACAGTGACACTGTTGGGCAATCGTCCACTACATCATGAAATAATGAA 483
Qy 477 GCGAATGCTGATGTTTAAAGCGATGGTAGAGATAACAGCTGTATGATCTCGAAAGC 536
Db 484 GCGAATGCTGATGTTTAAAGCGATGGTAGAGATAACAGCTGTATGATCTCGAAAGC 543
Qy 537 CCGTGACCCCGACACACAGGAGCGCGCAGTGAGTCTCGGCGCTTGTGACACAGGG 596
Db 544 CCGTGACCCCGACACACAGGAGCGCGCAGTGAGTCTCGGCGCTTGTGACACAGGG 602
Qy 597 GGGAGCGCAGGAGACAGCTGTGTGGCCATCATCTGCATACGGTGGGCGGTGTTGTCGAG 656
Db 603 GGGAGCGCAGGAGACAGCTGTGTGGCCATCATCTGCATACGGTGGGCGGTGTTGTCGAG 662
Qy 657 AGGATGTGTCTATCGGTGTAGGACACAGCGGTGGCACTTTATAAAGCCCACTAAACAG 716
Db 663 AGGATGTGTCTATCGGTGTAGGACACAGCGGTGGCACTTTATAAAGCCCACTAAACAG 722
Qy 717 TCCAGAGAGCAGACACACCGCGCAAGGGAGGTCAAGGCTTCTGTTGGCAGATTT 776
Db 723 TCCAGAGAGCAGACACACCGCGCAAGGGAGGTCAAGGCTTCTGTTGGCAGATTT 782
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RESULT 5

US-10-023-282-56

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; Sequence 56, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,919
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 56
; LENGTH: 1603
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (336)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (341)

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; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (788)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-023-282-56

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Query Match          92.7%; Score 1196.6; DB 5; Length 1603;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1268; Conservative 5; Mismatches 13; Indels 9; Gaps 6;

Qy 1  CCCACGGCTCCGGCCCGCCCGCTCCGGAGCGGCTCTCCCTTCCGAGCGGGACGGCGGC 60
Db 7  CCCACGGCTCCGGCCCGCCCGCTCCGGAGCGGCTCTCCCTTCCGAGCGGGAC--CGGC 64

Qy 61 GCCCTGGGGAGGAGGCGCGAAGCGACGCGCGATGGCTCCGCGGGCACTCCCGGGGTCCG 120
Db 65 GCCCTGGGGAGGAGGCGCGA--CGACGCGCGATGGCTCCGCGGGCACTCCCGGGGTCCG 123

Qy 121 CGCTCCTAGCGGCTGCTGCTTTCGTGGGAGCGCGTGAAGTTCGCCGCTGGTGGCTCCGG 180
Db 124 CGCTCCTAGCGGCTGCTGCTTTCGTGGGAGCGCGTGAAGTTCGCCGCTGGTGGCTCCGG 183

Qy 181 ACAATGGGAGCAGCGCACATTTGCATCCAGAAACAGAGACGACCGCTCCGCCAGCAACG 240
Db 184 ACAATGGGAGCAGCGCACATTTGCATCCAGAAACAGAGACGACCGCTCCGCCAGCAACG 243

Qy 241 ATACTGGGAATGGAACACCCAGAAATATATTCATACGCGCTTGTCCCTGTGTTCTTTATCA 300
Db 244 ATACTGGGAATGGAACACCCAGAAATATATTCATACGCGCTTGTCCCTGTGTTCTTTATCA 303

Qy 301 TGGGTCTCTTTGGCGTCTCTCAITTTGCCACCTGC---TTAAGAGAAGAGGTATCGTTGTA 357
Db 304 TGGGTCTCTTTGGCGTCTCTCAITTTGCCACCTGC---TTAAGAGAAGAGGTATCGTTGTA 363

Qy 358 CAACAGAGCAGAGCAAGATATCGAAGAGG--AAAAGGTTGAAAAGATAGAAATGAATGAC 416
Db 364 CAACAGAGCAGAGCAAGATATCGAAGAGGAAAAGGTTGAAAAGATAGAAATGAATGAC 423

Qy 417 AGTGTGAATGAAAACAGTGAACACTGTTGGGCAATCGTCCACTACATCATGAAATAAGAA 476
Db 424 AGTGTGAATGAAAACAGTGAACACTGTTGGGCAATCGTCCACTACATCATGAAATAAGAA 483

Qy 477 GCGAATGCTGATGCTCTTTAAAGGCGATGGTAGAGATAACAGCCTGTATGATCTCTGAAGC 536
Db 484 GCGAATGCTGATGCTCTTTAAAGGCGATGGTAGAGATAACAGCCTGTATGATCTCTGAAGC 543

Qy 537 CCGGTGACCCCGCAGCACACCGAGGAGCCCGCCAGTGAAGTCTGGGCGCTTTGTCAACAGGG 596
Db 544 CCGGTGACCCCGCAGCACACCGAGGAGCCCGCCAGTGAAGTCTGGG--CTTTGTCAACAGGG 602

Qy 597 GGGACGCCAGGGAAAGCAAGTCTGTGGCCATCATCTGCGCATACGCGTGGCGGTGTGTGCGAG 656
Db 603 GGGACGCCAGGGAAAGCAAGTCTGTGGCCATCATCTGCGCATACGCGTGGCGGTGTGTGCGAG 662

Qy 657 AGGGATGTGTGTCATCGGTGTAGGCAACAGCGGTGGCACTTTTATAAGCCCACTTAACAAG 716
Db 663 AGGGATGTGTGTCATCGGTGTAGGCAACAGCGGTGGCACTTTTATAAGCCCACTTAACAAG 722

Qy 717 TCCAGAGAGAGCAGACACCGCGCCCAAGGCGAGGTCAACGCTCTTCTTGTGGCAGATTT 776
Db 723 TCCAGAGAGAGCAGACACCGCGCCCAAGGCGAGGTCAACGCTCTTCTTGTGGCAGATTT 782

Qy 777 AGAGTTACAAAAGTGGAGCACAAGTCAAAACAGAAAGAAACGAGAGCCCTGATGTGTGTT 836
Db 783 AGAGTTACAAAAGTGGAGCACAAGTCAAAACAGAAAGAAACGAGAGCCCTGATGTGTGTT 842

Qy 837 AGTGGGCTGAAACCGTCAATGGGAGGTGCCCGGCAACACCTGTGAAGAGAGACGCGAGT 896
Db 843 AGTGGGCTGAAACCGTCAATGGGAGGTGCCCGGCAACACCTGTGAAGAGAGACGCGAGT 902

Qy 897 GGCAACAGAGTAGCAGGTGAGCCGCTGTTTGGTGACATTTGGGGCGCAGAGTGGTGACGGGT 956
Db 897 GGCAACAGAGTAGCAGGTGAGCCGCTGTTTGGTGACATTTGGGGCGCAGAGTGGTGACGGGT 956

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Db 903 GGCACAGTAGCAGGTGAGCGGTGTTTTCGTGACATTTGGGCGACAGTGGTGCAGGTT 962
Qy 957 GAGGAGAAGTACTTTGGAGCCTCCAGGTCTGTGGCAGCATAGGAATGGTATTTCACAG 1016
Db 963 GAGGAGAAGTACTTTGGAGCCTCCAGGTCTGTGGCAGCATAGGAATGGTATTTCACAG 1022
Qy 1017 GGAAGTGGGAGAGCTTTCTTGAACCCAGGAGACTGAGGGGACTGAACATGATTACTTTG 1076
Db 1023 GGAAGTGGGAGAGCTTTCTTGAACCCAGGAGACTGAGGGGACTGAACATGATTACTTTG 1082
Qy 1077 TCTGCTAGAGCTTTCTTGAAGAAAGTCAAAAATTAGTGCCTCCAGGGGCTTGGCCGTGT 1136
Db 1083 TCTGCTAGAGCTTTCTTGAAGAAAGTCAAAAATTAGTGCCTCCAGGGGCTTGG-CTGT 1141
Qy 1137 GTGATAATGAGATAGAGGATTACTTTGTGAGGCAATGTGGCATGTGGGATTTGGGCAA 1196
Db 1142 GTGATAATGAGATAGAGGATTACTTTGTGAGGCAATGTGGCATGTGGGATTTGGGCAA 1201
Qy 1197 ACTAGAATTACATCACCCACCATATAGGGCTTGCATTACCAGGAGGAGAAAGCACCTA 1256
Db 1202 ACTAGAATTACATCACCCACCATATAGGGCTTGCATTACCAGGAGGAGAAAGCACCTA 1261
Qy 1257 GTGTTGCTGCATCTTTTACGCAAAAAA 1291
Db 1262 GTGTTGCTGCATCTTTTACGCAAAAAA 1296

RESULT 6
US-09-925-065A-84619
; Sequence 84619, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925.065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84619
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-84619

Query Match 17.5%; Score 226.2; DB 4; Length 591;
Best Local Similarity 98.7%; Pred. No. 1.2e-57;
Matches 228; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 175 CTCGGACAAATGGGAGCGCCGACATTGCACTCCAGAACAGACGACCCCGTCGCCCA 234
Db 111 CTGTAGACAAATGGGAGCGCCGACATTGCACTCCAGAACAGACGACCCCGTCGCCCA 170
Qy 235 GCAACGATACCTGGGAATGGACACCCAGNATATATTCATAGCGCTTGTCCCTGTGTCT 294
Db 171 GCAACGATACCTGGGAATGGACACCCAGNATATATTCATAGCGCTTGTCCCTGTGTCT 230
Qy 295 TTATCATGGGTCTCTTTGGCGTCTCTATTTCGCCACCTGCTTAAAGAAAGGCTATCGTT 354
Db 231 TTATCATGGGTCTCTTTGGCGTCTCTATTTCGCCACCTGCTTAAAGAAAGGCTATCGTT 290
Qy 355 GTACAACAGAACGACAGCAAGATATCGAAGAGGAAAGGTTTGAAGAGATAG 405

Db 291 GTACACAGAACGACAGCAAGATATCGAAGAGGAAAGGTTTGAAGAGATAG 341
RESULT 7
US-10-363-345A-5597
; Sequence 5597, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363.345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 5597
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 5597
US-10-363-345A-5597

Query Match 8.9%; Score 115.4; DB 8; Length 694;
Best Local Similarity 81.2%; Pred. No. 6.4e-24;
Matches 134; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 16 CGCCGGCTCCGGAGCGGCTCTGCCCTTCCGAGCGGGACGCGGCCCTCGGGGAGGAG 75
Db 246 CGTCGGTTTCGAGCGGTTTGTGTTTTTCGAGCGGGACGCGGCTTTTGGGGAGGAG 305
Qy 76 GCGAAGCGAGCGCGGATGCTCCGGGGCACTCCCGGGGTCCGCCCTCTAGCCGCTG 135
Db 306 GCGAAGCGAGCGCGGATGCTTCCGGGGTATTTTCGGGGTTCGTCGTTTAGTCGTTG 365
Qy 136 CTGCTTTCTGTTGGAGCGCGCTGAGTTCCGCCCTGTTGGCTCCCG 180
Db 366 TTGTTTTCTGTTGGAGCGGCTCGTGTGTTGTTGGTTTCGG 410

RESULT 8
US-10-363-345A-5598/C
; Sequence 5598, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363.345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 5598
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 5598
US-10-363-345A-5598

Query Match 8.9%; Score 115.4; DB 8; Length 694;
Best Local Similarity 81.2%; Pred. No. 6.4e-24;
Matches 134; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 16 CGCCGGCTCCGGAGCGGCTCTGCCCTTCCGAGCGGGACGCGGCCCTCGGGGAGGAG 75

Db 449 CGTCGGTTCCGAGCGGTTTGTGTTTTCGAGCGCGGACGCGCGGTTTGGGGAGGAG 390
QY 76 GCGGAGCGACGGCGCATGGCTCCGGGGGACATCCCGGGGTCCGCGTCTACCCGCTG 135
Db 389 GCGGAGCGACGGCGCATGGTTTCGGGGGTATTTTCGGGGTTCGTCGTTTAGTCGTTG 330
QY 136 CTGCTCTCGTGGGAGGCGCGTGAAGTTCCGCGCTGGTGGCTCCGG 180
Db 329 TTGTTTTCGTGGGAGGCGTCGTGAGTTCGTCGTTGGTGGTTTCGG 285

RESULT 9

US-10-363-483A-5597
; Sequence 5597, Application US/10363483A
; Publication No. US2005006401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363.483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 5597
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 5597
US-10-363-483A-5597

Query Match 8.9%; Score 115.4; DB 9; Length 694;
Best Local Similarity 81.2%; Pred. No. 6.4e-24;
Matches 134; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 16 CGCGCGCTCCGAGCGGCTGCTCCGAGCGCGGACGCGCGGCTGGGGAGGAG 75
Db 246 CGTCGGTTCCGAGCGGTTTGTGTTTTCGAGCGCGGACGCGCGGTTTGGGGAGGAG 305
QY 76 GCGGAGCGACGGCGCATGGCTCCGCGGACATCCCGGGTCCGCGTCTAGCCGCTG 135
Db 306 GCGGAGCGACGGCGCATGGTTTCGGGGGTATTTTCGGGGTTCGTCGTTTAGTCGTTG 365
QY 136 CTGCTCTCGTGGGAGGCGCGTGAAGTTCCGCGCTGGTGGCTCCGG 180
Db 366 TTGTTTTCGTGGGAGGCGTCGTGAGTTCGTCGTTGGTGGTTTCGG 410

RESULT 10

US-10-363-483A-5598/c
; Sequence 5598, Application US/10363483A
; Publication No. US2005006401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363.483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 5598
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 5598
US-10-363-483A-5598

Query Match 8.9%; Score 115.4; DB 9; Length 694;
Best Local Similarity 81.2%; Pred. No. 6.4e-24;
Matches 134; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 16 CGCGCGCTCCGAGCGGCTGCTCCGAGCGCGGACGCGCGGCTGGGGAGGAG 75
Db 449 CGTCGGTTCCGAGCGGTTTGTGTTTTCGAGCGCGGACGCGCGGTTTGGGGAGGAG 390
QY 76 GCGGAGCGACGGCGCATGGCTCCGCGGACATCCCGGGGTCCGCGTCTACCCGCTG 135
Db 389 GCGGAGCGACGGCGCATGGTTTCGGGGGTATTTTCGGGGTTCGTCGTTTAGTCGTTG 330
QY 136 CTGCTCTCGTGGGAGGCGCGTGAAGTTCCGCGCTGGTGGCTCCGG 180
Db 329 TTGTTTTCGTGGGAGGCGTCGTGAGTTCGTCGTTGGTGGTTTCGG 285

RESULT 11

US-10-363-345A-5599/c
; Sequence 5599, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363.345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 5599
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 5599
US-10-363-345A-5599

Query Match 8.1%; Score 104.6; DB 8; Length 694;
Best Local Similarity 73.2%; Pred. No. 1.2e-20;
Matches 134; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 2 CCACGGCTCCGCGCGGCTCCGAGCGGCTGCTGCTTCCGAGCGCGGACGCGGCG 61
Db 463 CCACTCGATCAACCCGCGGACTCCGAAACGACTCTACCTTCCCGAACGCGGACG 404
QY 62 CCCTGGGGAGGAGGCGGAGCGACGCGGCGATGGCTCCCGGGGCACTCCCGGGTCCGC 121
Db 403 CCCTAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 344
QY 122 CGTCCTAGCGGCTGCTGCTTTCGTTGGGAGGCGCGGTGAGTTCCGCGTGGTCCGGA 181
Db 343 CGTCCTAACCGCTACTATCTTCGTAAAAAGCGCGTAATTCGCCGCTAATACTCCGAA 284
QY 182 CAA 184
Db 283 TAA 281

RESULT 12

US-10-363-345A-5600
; Sequence 5600, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
US-10-363-345A-5600

; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 5600
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 5600
US-10-363-345A-5600

Query Match 8.1%; Score 104.6; DB 8; Length 694;
Best Local Similarity 73.2%; Pred. No. 1.2e-20;
Matches 134; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 2 CCACGCGTCCGGCGCGGCTCCGGAGCGGCTCTGCTTCCCGAGCGCGGAGCGCGCG 61
DB 232 CCACCTCGATCAACCGCGGACTCCGAAACGACTTACCTTCCCGAACGCGAAACGCGACG 291
QY 62 CCCTGGGGAGGAGGCGAAGCGACGCGCGGCGATCGGCTCCGGGGCACTTCCCGGGTCCGC 121
DB 292 CCCTTAAAAAAGAAAAACGAAACGACGCGACGATTAACCTCCGGAACACTTCCCGAAATCCGC 351
QY 122 CGTCTAGCCGCTGCTGCTTCTCGTGGGAGGCGCGTGTGCTGCGCGCTGGTGGCTCCGGA 181
DB 352 CGTCTAACCGCTACTATCTTTCGTAAGAAACGCGGTAATTCGCGCTAATAACTCCGAA 411
QY 182 CAA 184
DB 412 TAA 414

RESULT 13

US-10-363-483A-5599/c
; Sequence 5599, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 5599
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 5599
US-10-363-483A-5599

Query Match 8.1%; Score 104.6; DB 9; Length 694;
Best Local Similarity 73.2%; Pred. No. 1.2e-20;
Matches 134; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 2 CCACGCGTCCGGCGCGGCTCCGGAGCGGCTCTGCTTCCCGAGCGCGGAGCGCGCG 61
DB 463 CCACCTCGATCAACCGCGGACTCCGAAACGACTTACCTTCCCGAACGCGAAACGCGACG 404
QY 62 CCCTGGGGAGGAGGCGAAGCGACGCGCGATCGGCTCCGGGGCACTTCCCGGGTCCGC 121
DB 403 CCCTTAAAAAAGAAAAACGAAACGACGCGACGATTAACCTCCCGGAACACTTCCCGAAATCCGC 344
QY 122 CGTCTAGCCGCTGCTGCTTCTCGTGGGAGGCGCGTGTGCTGCGCGCTGGTGGCTCCGGA 181
DB 343 CGTCTAACCGCTACTATCTTTCGTAAGAAACGCGGTAATTCGCGCTAATAACTCCGAA 284
QY 182 CAA 184

DB 283 TAA 281

RESULT 14

US-10-363-483A-5600
; Sequence 5600, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 5600
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 5600
US-10-363-483A-5600

Query Match 8.1%; Score 104.6; DB 9; Length 694;
Best Local Similarity 73.2%; Pred. No. 1.2e-20;
Matches 134; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 2 CCACGCGTCCGGCGCGGCTCCGGAGCGGCTCTGCTTCCCGAGCGCGGAGCGCGCG 61
DB 232 CCACCTCGATCAACCGCGGACTCCGAAACGACTTACCTTCCCGAACGCGAAACGCGACG 291
QY 62 CCCTGGGGAGGAGGCGAAGCGACGCGCGATCGGCTCCGGGGCACTTCCCGGGTCCGC 121
DB 292 CCCTTAAAAAAGAAAAACGAAACGACGCGACGATTAACCTCCCGGAACACTTCCCGAAATCCGC 351
QY 122 CGTCTAGCCGCTGCTGCTTCTCGTGGGAGGCGCGTGTGCTGCGCGCTGGTGGCTCCGGA 181
DB 352 CGTCTAACCGCTACTATCTTTCGTAAGAAACGCGGTAATTCGCGCTAATAACTCCGAA 411
QY 182 CAA 184
DB 412 TAA 414

RESULT 15

US-09-925-065A-2551
; Sequence 2551, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2551
; LENGTH: 2205

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-2551

Query Match      5.7%; Score 74; DB 4; Length 2205;
Best Local Similarity 100.0%; Pred. No. 4.4e-11;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      404 AGAATTGAATGACAGTGTGGAATGAAACAGTGCACACTGTTGGGCAAAATCGTCCACTACAT 463
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      159 AGAATTGAATGACAGTGTGGAATGAAACAGTGCACACTGTTGGGCAAAATCGTCCACTACAT 218
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy      464 CATGAAAAATGAAG 477
         ||||||||||||||
Db      219 CATGAAAAATGAAG 232
         ||||||||||||||
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Search completed: February 23, 2006, 17:25:18
Job time : 1205 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 15:08:27 ; Search time 442 Seconds
(without alignments)
6228.248 Million cell updates/sec

Title: US-10-620-562-1
Perfect score: 1291
Sequence: 1 cccacggtccgcccgcg.....cttacgcaaaaaaaaaa 1291

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:

- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	226.2	17.5	591	US-09-925-065A-84619	Sequence 84619, A
2	74	5.7	2205	US-09-925-065A-2551	Sequence 2551, Ap
3	74	5.7	2205	US-09-925-065A-2552	Sequence 2552, Ap
4	74	5.7	2205	US-09-925-065A-2553	Sequence 2553, Ap
5	74	5.7	2480	US-09-925-065A-720502	Sequence 720502, A
6	74	5.7	2480	US-09-925-065A-720503	Sequence 720503, A
7	74	5.7	2480	US-09-925-065A-720504	Sequence 720504, A
8	74	5.7	2480	US-09-925-065A-720505	Sequence 720505, A
9	58.6	4.5	2638	US-11-042-814-1	Sequence 1, Appli
10	50.6	3.9	2479	US-11-042-814-3	Sequence 3, Appli
11	46.6	3.6	1155	US-09-925-065A-38365	Sequence 38365, A
12	45	3.5	1731	US-11-052-554A-548	Sequence 548, App
13	42.6	3.3	1189	US-10-085-877-29	Sequence 29, Appl
14	41.6	3.2	811	US-09-925-065A-28354	Sequence 28354, A
15	41.6	3.2	811	US-09-925-065A-28355	Sequence 28355, A
16	40.8	3.2	3075	US-09-925-065A-184526	Sequence 184526, A
17	40	3.1	5075	US-11-000-688-1133	Sequence 1133, Ap
18	40	3.1	5099	US-10-821-234-193	Sequence 193, App
19	39.8	3.1	3370	US-10-972-053-3	Sequence 3, Appli
20	39.2	3.0	172147	US-11-112-908-22	Sequence 22, Appli

c	21	39.2	3.0	186682	12	US-11-112-908-23	Sequence 23, Appl
c	22	39	3.0	47460	12	US-11-124-368A-2877	Sequence 2877, Ap
c	23	38.8	3.0	30140	12	US-11-052-544-29	Sequence 29, Appl
c	24	38.8	3.0	38703	12	US-11-052-544-28	Sequence 28, Appl
c	25	38.4	3.0	587	6	US-09-925-065A-320868	Sequence 320868, A
c	26	38	2.9	383	6	US-09-925-065A-562024	Sequence 562024, A
c	27	38	2.9	452	6	US-09-925-065A-644775	Sequence 644775, A
c	28	38	2.9	153376	12	US-11-121-086-5	Sequence 5, Appli
c	29	38	2.9	172543	12	US-11-121-086-6	Sequence 6, Appli
c	30	37.8	2.9	645179	8	US-10-995-561-13293	Sequence 13293, A
c	31	37.6	2.9	289	6	US-09-925-065A-499724	Sequence 499724, A
c	32	37.6	2.9	622	6	US-09-925-065A-862767	Sequence 862767, A
c	33	37.6	2.9	3500	12	US-11-085-775-1	Sequence 1, Appli
c	34	37.2	2.9	587	6	US-09-925-065A-320869	Sequence 320869, A
c	35	36.8	2.9	3657	9	US-11-072-512-352	Sequence 352, App
c	36	36.6	2.8	607	6	US-09-925-065A-767166	Sequence 767166, A
c	37	36.6	2.8	2458	8	US-10-947-249-2	Sequence 2, Appli
c	38	36.6	2.8	2458	8	US-10-947-249-3	Sequence 3, Appli
c	39	36.6	2.8	2825	12	US-11-136-527-192	Sequence 192, App
c	40	36.6	2.8	22970	7	US-10-467-033-25	Sequence 25, Appl
c	41	36.6	2.8	22970	7	US-10-467-033-26	Sequence 26, Appl
c	42	36.4	2.8	1754	12	US-11-136-527-2453	Sequence 2453, Ap
c	43	36.4	2.8	3167	6	US-09-925-065A-21764	Sequence 21764, A
c	44	36.2	2.8	602	6	US-09-925-065A-493497	Sequence 493497, A
c	45	36.2	2.8	602	6	US-09-925-065A-493498	Sequence 493498, A

ALIGNMENTS

RESULT 1
US-09-925-065A-84619
; Sequence 84619, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84619
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-84619

Query Match	17.5%	Score	226.2	DB	6	Length	591
Best Local Similarity	99.7%	Pred. No.	5e-53				
Matches	228	Conservative	0	Mismatches	3	Indels	0
Gaps	0						
Qy	175	CTCCGGCAATGGGAGCAGCGGCACATTGGCACTCCAGACAGACAGACCCCGTGGCCCA	234				
Db	111	CTGTAGCAATGGGAGCAGCGGCACATTGGCACTCCAGACAGACAGACCCCGTGGCCCA	170				
Qy	235	GCAACGATATCGGGAATGGACACCCAGAGATATATGATACCGCTTGTCTGTCTGTCT	294				
Db	171	GCAACGATATCGGGAATGGACACCCAGAGATATATGATACCGCTTGTCTGTCTGTCT	230				
Qy	295	TTATCATGGGTCTCTTTGGCGTCTCTATTTGCCACCTGCTTAAAGAAAGGCTATCGTT	354				

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Db      231 TTATCATGGGCTCTTTGGCGCTCTCAATTCCTCCACCTGCTTTAAGAAGAAAGGCTATCGTT 290
Qy      355 GTACAACAGACGACGACAGATATCGAAGAGGAAAGGTTGAAAGATAG 405
Db      291 GTACACAGAACGACGACGATATCGAAGAGGAAAGGTTGAAAGATAG 341

RESULT 2
US-09-925-065A-2551
; Sequence 2551, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2551
; LENGTH: 2205
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-2551

Query Match      5.7%; Score 74; DB 6; Length 2205;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      404 AGAATTGAATGACAGTGTGAATGAAACACGTGACACTGTTGGGCAAAATCGTCCACTACAT 463
Db      159 AGAATTGAATGACAGTGTGAATGAAACACGTGACACTGTTGGGCAAAATCGTCCACTACAT 218

Qy      464 CATGAAAAATGAAG 477
Db      219 CATGAAAAATGAAG 232

RESULT 3
US-09-925-065A-2552
; Sequence 2552, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2552
; LENGTH: 2205
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-2552

Query Match      5.7%; Score 74; DB 6; Length 2205;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      404 AGAATTGAATGACAGTGTGAATGAAACACGTGACACTGTTGGGCAAAATCGTCCACTACAT 463
Db      159 AGAATTGAATGACAGTGTGAATGAAACACGTGACACTGTTGGGCAAAATCGTCCACTACAT 218

Qy      464 CATGAAAAATGAAG 477
Db      219 CATGAAAAATGAAG 232

RESULT 4
US-09-925-065A-2553
; Sequence 2553, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2553
; LENGTH: 2205
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-2553

Query Match      5.7%; Score 74; DB 6; Length 2205;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      404 AGAATTGAATGACAGTGTGAATGAAACACGTGACACTGTTGGGCAAAATCGTCCACTACAT 463
Db      159 AGAATTGAATGACAGTGTGAATGAAACACGTGACACTGTTGGGCAAAATCGTCCACTACAT 218

Qy      464 CATGAAAAATGAAG 477
Db      219 CATGAAAAATGAAG 232

RESULT 5
US-09-925-065A-720502
; Sequence 720502, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
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; LENGTH: 2205
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-2552

Query Match      5.7%; Score 74; DB 6; Length 2205;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      404 AGAATTGAATGACAGTGTGAATGAAACACGTGACACTGTTGGGCAAAATCGTCCACTACAT 463
Db      159 AGAATTGAATGACAGTGTGAATGAAACACGTGACACTGTTGGGCAAAATCGTCCACTACAT 218

Qy      464 CATGAAAAATGAAG 477
Db      219 CATGAAAAATGAAG 232

RESULT 4
US-09-925-065A-2553
; Sequence 2553, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
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; LENGTH: 2205
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-2553

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Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      464 CATGAAAAATGAAG 477
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US-09-925-065A-720502
; Sequence 720502, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
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; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 720502
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-925-065A-720502

Query Match          5.7%; Score 74; DB 6; Length 2480;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 464 CATGAAAAATGAAG 477
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RESULT 6
US-09-925-065A-720503
; Sequence 720503, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
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US-09-925-065A-720503

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RESULT 7
US-09-925-065A-720504
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; Sequence 720504, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
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; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 720504
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US-09-925-065A-720504

Query Match          5.7%; Score 74; DB 6; Length 2480;
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Db 494 CATGAAAAATGAAG 507

RESULT 8
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; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 720505
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-925-065A-720505

Query Match          5.7%; Score 74; DB 6; Length 2480;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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4	900	69.7	1320	6	CS051293	CS051293 Sequence
5	900	69.7	1320	6	AX136257	AX136257 Sequence
6	900	69.7	1320	8	AK075468	AK075468 Homo sapi
7	899	69.6	1364	8	BC039540	BC039540 Homo sapi
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9	685.2	53.1	726	6	CS051580	CS051580 Sequence
10	685.2	53.1	726	6	AX136544	AX136544 Sequence
11	680	52.7	680	6	CQ727837	CQ727837 Sequence
12	622.2	48.2	2581	9	BC031198	BC031198 Mus muscu
13	620.6	48.1	2481	9	BC066137	BC066137 Mus muscu
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15	519.6	40.2	161070	8	AC027607	AC027607 Homo sapi
16	519.6	40.2	171279	14	AC036185	AC036185 Homo sapi
17	355.2	27.5	3672	5	AJ851746	AJ851746 Gallus ga
18	353.2	27.4	1166	5	CR523601	CR523601 Gallus ga

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05-SEP-1997 US	60/057661, 05-SEP-1997 US	60/057647 PR
18-DEC-1997 US	60/070923	
PI PAUL YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A ROSEN,		
PI JING SHAN HU, HENRIK S OLSEN, REINHARD EBNER, LAURIE A BREWER, PI PAUL A MOORE,		
PI YANGGU SHI, CHARLES FLORENCE, KIMBERLY FLORENCE, DAVID W LAFLEUR, JIAN NI,		
PI PING FAN, YING FEI WEI, CARRIE L FISCHER, DANIEL R SOPPET, YI LI, ZHIZHEN ZENG,		
PI HLA KYAW, GUO LIANG YU, PING FENG, PATRICK J DILLON, GREGORY A PI ENDRESS,		
PI KENNETH C CARTER		
PC A01N37/18, A01N43/04, C12Q1/00, C12Q1/02, C12Q1/68, C12N5/00 PC		
C12N5/06, C12N15/00,		
PC C12N15/06 C12N15/09, C12N15/10, C12N15/11, G01N33/53 CC		
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CC Topology: Linear;		
FH Key Location/Qualifiers.		
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QY	61 GCCTTGGGAGGAGGCGGAGCGACGCGCGGATGGCTCCGCGGCACTCCCGGGTCCG 120	
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QY	121 CCGTCTAGCGCTGCTGCTCTCGTGGAGCGCGCGGTGAGTTCGCGCTGCGTCCCG 180	
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QY	358 CAACAGAGCAGAGCAAGATATCGAAGAGG-AAAGGTTGAAAGATAGAAATGAATGAC 416	
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QY	417	AGTGTGAATGAAAA	CAGTGACACTGTTGGGCAAAATCGTCCACTACATCATGAAAAATGAA	476
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QY	477	GCGAATGCTGATGCTT	TAAAGGCGATGTTAGCAGATACAGCCTGTATGATCTCTGAAAGC	536
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QY	537	CCCGTGACCCCGCAGCACAC	AGGAGCGCGCCAGTGAAGTCTCTGGGCCCTTTGTACACAGGG	596
Db	544	CCCGTGACCCCGCAGCACAC	AGGAGCGCGCCAGTGAAGTCTCTGGGCCCTTTGTACACAGGG	602
QY	597	GCGACGCCAGGAAGCAGCTGT	GTGGCCATCATCTGCATACAGGTGGGCGGTGTGTCGAG	656
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QY	717	TCCAGAGAGCAGACACCGCG	CCCAAGGCGAGGTCAAGTCTCTTCTGTGGCAGATTT	776
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QY	897	GGCAGAGTAGCAGGTGAGCC	GTGCTGTTTGGTGAACATTTGGGGGCGAGCTGGTGCAGGGT	956
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QY	957	GAGGAGAGGTACTTTGGAG	CCCTCCAGGTGCTGTGGCAGCATAGGAATGGTATTTGCACAG	1016
Db	963	GAGGAGAGGTACTTTGGAG	CCCTCCAGGTGCTGTGGCAGCATAGGAATGGTATTTGCACAG	1022
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	Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;			

Hominidae; Homo.

REFERENCE
1
AUTHORS
Young, P., Greene, J.M., Ferrie, A.M., Ruben, S.M., Rosen, C.A.,
Hu, J.S., Olsen, H.S., Ebner, R., Brewer, L.A., More, P.A., Shi, Y.,
Florence, C., Florence, K., Lapleur, D.W., Ni, J., Fan, P., Wei, Y.F.,
Fischer, C.L., Soppet, D.R., Li, Y., Zeng, Z., Kyaw, H., Yu, G.L.,
Feng, P., Dillon, P.J., Endress, G.A. and Carter, K.C.
207 human secreted proteins
Patent: EP 1428833-A 56 16-JUN-2004;
Human Genome Sciences, Inc. (US)

TITLE
JOURNAL
FEATURES
Location/Qualifiers
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Query Match 92.7%; Score 1196.6; DB 6; Length 1603;
Best Local Similarity 97.9%; Pred. No. 1.8e-276;
Matches 1268; Conservative 5; Mismatches 13; Indels 9; Gaps 6;
Qy 1 CCCAGCGCTCCGGCCCGCGGCTCGGAGCGGCTCTGCGCTCCGAGCGCGGAGCGGCG 60
Db 7 CCCAGCGCTCCGGCCCGCGGCTCGGAGCGGCTCTGCGCTCCGAGCGCGGAG--CCGC 64
Qy 61 GCCCTGGGGAGGAGGCGGAGCGGAGCGGCGGAGCGGCTCCGCGGCGCTCCGCGGCTCCG 120
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Qy 121 CCGTCTAGCGCTGCTCTCTTCTGGGAGGCGCGCTGAGTTCGCGCGTGGTCTCCGG 180
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RESULT 3
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LOCUS
DEFINITION
Secretory protein or membrane protein.
ACCESSION
BD123581
VERSION
BD123581.1 GI:23218526
KEYWORDS
JP 2002017376-A/90.
SOURCE
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ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 1320)
Ota, T., Iwagaki, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
Hayashi, K.
TITLE
JOURNAL
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Patent: JP 2002017376-A 90 22-JAN-2002;
HELIX RESEARCH INSTITUTE
COMMENT
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PN JP 2002017376-A/90
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253173
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SUGIYAMA
PI KOJI HAYASHI
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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Best Local Similarity	99.4%; Pred. No. 3.2e-205;	
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QY	64	CTGGGGAGGAGGCGGAAGCAGCGCGATGGCTCCGCGGCACTCCCGGGTCCGCGG 123
Db	61	CTGGGGAGGAGGCGGAAGCAGCGCGATGGCTCCGCGGCACTCCCGGGTCCGCGG 120
QY	124	TCCTAGCGCTGCTCTTCTGTTGGAGGCGCGTGGTTCGCGCTGCTCGCGGCTCCGCGG 183
Db	121	TCCTAGCGCTGCTGCTCTTCTGTTGGAGGCGCGTGGTTCGCGCTGCTCGCGGCTCCGCGG 180
QY	184	ATGGGAGCAGCCGACATTTGCATCCAGAACAGACAGACCCCGCTCGCCAGCAACGATA 243
Db	181	ATGGGAGCAGCCGCGCATTTGCATCCAGAACAGACAGACCCCGCTCGCCAGCAACGATA 240
QY	244	CTGGGAATGGACACCCAGAAATATTTGCATACCGGCTTGTCCCTGTTCTTTATCATGG 303
Db	241	CTGGGAATGGACACCCAGAAATATTTGCATACCGGCTTGTCCCTGTTCTTTATCATGG 300
QY	304	GTCTCTTTGGCGTCTCATTTGCCCTCTTAAAGAAAGGCTATCGTTGTGTACACAG 363
Db	301	GTCTCTTTGGCGTCTCATTTGCCCTCTTAAAGAAAGGCTATCGTTGTGTACACAG 360
QY	364	AAGCAGACAGATATCGAAGAGGAAAAGTTGAAAAGATAGAAATTTGAATGACAGTGTGA 423
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Query Match	69.7%; Score 900; DB 6; Length 1320;	
Best Local Similarity	99.4%; Pred. No. 3.2e-205;	
Matches	903; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
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Db	61	CTGGGGAGGAGGCGGAAGCAGCGCGATGGCTCCGCGGCACTCCCGGGTCCGCGG 120
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QY	184	ATGGGAGCAGCCGACATTTGCATCCAGAACAGACAGACCCCGCTCGCCAGCAACGATA 243
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QY	364	AAGCAGACAGATATCGAAGAGGAAAAGTTGAAAAGATAGAAATTTGAATGACAGTGTGA 423
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QY	544	CCCCCAGCACACGAGGAGCCCGCAGTGAGTCTCGGGCCTTTGTTCACAGGGGGGACGC 603
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QY	724	AGAGCAGACCAAGCGGCAAGGGAGGTCAAGGTCCTTTCTGTGGCAGATTTAGAGTTA 783
Db	721	AGAGCAGACCAAGCGGCAAGGGAGGTCAAGGTCCTTTCTGTGGCAGATTTAGAGTTA 780
QY	784	CAAAAGTGGAGCACAAGTCAAAACAGAGGAAACGAGAGCCGTGATCTGTAGTGGGG 843
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RESULT 5
AXI36257
LOCUS AXI36257 1320 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 179 from Patent EP1067182.
ACCESSION AXI36257
VERSION AXI36257.1 GI:14272663

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE 1
Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
Hayashi, K.
Secretory protein or membrane protein
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Helix Research Institute (JP)

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ORIGIN

Query Match 69.7%; Score 900; DB 6; Length 1320;
Best Local Similarity 99.4%; Pred. No. 3.2e-205;
Matches 903; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 4 ACGGTCCGGCCCGCGCTCCGAGCGGCTCTCCCTTCCGAGCGGGAGCGGGCGCC 63
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Qy 904 AGTAGCAG 911
Db 901 AGTAGCAG 908

RESULT 6
AK075468
LOCUS AK075468
DEFINITION Homo sapiens cdna P9EC0162 fis, clone PLACB1009772.

AK075468 1320 bp mRNA linear PRI 09-JUL-2005

ACCESSION	AK075468	
VERSION	AK075468.1	GI:22761572
KEYWORDS	oligo capping; fis (full insert sequence).	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Otsuki, T., Ota, T., Nishikawa, T., Hayashi, K., Suzuki, Y., Yamamoto, J., Wakamatsu, A., Kimura, K., Sakamoto, K., Hatano, N., Kawai, Y., Iehi, S., Saito, K., Kojima, S., Sugiyama, T., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Nagai, K., Sugano, S. and Isogai, T.	
TITLE	Signal Sequence and Keyword Trap in silico for Selection of Full-length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-Capped cDNA Libraries	
JOURNAL	DNA Res. 12, 117-126 (2005)	
REFERENCE	2	
AUTHORS	Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K., Iehi, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T., Nakamura, Y., Nagahari, K., Sugano, S. and Isogai, T.	
TITLE	HRI human cDNA sequencing project	
JOURNAL	Unpublished	
REFERENCE	3 (bases 1 to 1320)	
AUTHORS	Isogai, T. and Yamamoto, J.	
TITLE	Direct Submission	
JOURNAL	Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba, 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)	
COMMENT	HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing. Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.	
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ORIGIN	69.7%; Score 900; DB 8; Length 1320;	
Query Match	Best Local Similarity 99.4%; Pred. No. 3.2e-205;	
Matches	903; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
Qy	4 ACGCGTCCCGCCCGCGCTCCGAGCGGCTCTGCCTTCCGAGCGCGGACGGCGCC 63	
Db	1 ACTCGATCAGCCCGCGCTCCGAGCGGCTCTGCCTTCCGAGCGCGGACGGCGCC 60	
Qy	64 CTGGGGAGGAGGCGGAAGCGACCGCGCATGGCTCCCGCGGCACTCCCGGGTCCCGC 123	
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Qy	184 ATGGGAGCAGCGGCACATTGTCATCCAGAACAGAGACGACCCCGCTCGCCAGCAACGATA 243	

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Qy	304	GTCTCTTTGGCGTCTCATTTGCCACCTGCTTAAAGAGAAAGGCTATCGTTGTACAACAG	363
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Qy	604	CAGGAAAGCAGCTCTGTGGCCATCATCTGCATACGCTGGCGGTGTGTCTGAGAGGGATG	663
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Qy	664	TGTGTCATCGGTGTAGGACCAAGCGGTGGCACTTTATAAGCCCACTAAACAAGTCCAGAG	723
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Qy	784	CAAAAGTGGAGCAAGTCAAAACAGAAAGGAAACGAGAGCGCTGATGCTGTTAGTGGGG	843
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Qy	844	CTGAAACCGTCAATGGGGAGTGCAGCAACACCTGTGAAGAGAGACGAGTGGCACAG	903
Db	841	CTGAAACCGTCAATGGGGAGTGCAGCAACACCTGTGAAGAGAGACGAGTGGCACAG	900
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LOCUS	BC039540 1364 bp mRNA linear PRI 07-OCT-2003		
DEFINITION	Homo sapiens mRNA similar to expressed sequence AA536743 (CDNA clone MGC:50583 IMAGE:5748847), complete cds.		
ACCESSION	BC039540		
VERSION	BC039540.1		
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1364)		
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Sheetz, T.E., Brownstein, M.J., Udwin, T.B., Toshitake, S.,		


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COMMENT
OS Helix Research Institute
PN JP 2002017376-A/293
PD 22-JAN-2002
PF 07-JUL-2000 JP 20002531173
PI TOSHIO OTA, TAKAO ISOgai, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU
PI KOJI HAYASHI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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Best Local Similarity 98.3%; Pred. No. 1.2e-153;
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RESULT 9
CS051580 LOCUS CS051580 726 bp DNA linear PAT 23-MAR-2005
DEFINITION Sequence 466 from Patent EP1514933.
ACCESSION CS051580
VERSION CS051580.1 GI:61890757
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
MAMMALIA; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Hayaishi, K.
TITLE Secretory protein or membrane protein
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Research Association for Biotechnology (JP)
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QY 184 ATGGGAGCAGCCGACATTCGACTCCAGAACAGAGACGACCCCGTCCGCGAACGATA 243
DB 181 ATGGGAGCAGCCGCGCATTCGACTCCAGAACAGAGACGACCCCGTCCGCGAACGATA 240
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QY 603 CCAGGGAAGCAGCTCTGTGGCCATCATCTGCATACGCTGGCGGTGTTGTCGAGAGGAT 662
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Qy 722 AGAG 725
Db 721 AGAG 724

RESULT 10
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LOCUS AX136544 726 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 466 from Patent EP1067182.
ACCESSION AX136544
VERSION AX136544.1 GI:14272948
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 466 10-JAN-2001;
Helix Research Institute (JP)
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Best Local Similarity 98.3%; Pred. No. 1.2e-153;
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Db 361 AAGCAGGCAAGATATCGAGAGGAAAGGTTGAAGATAGATTTGAATGACAGTGTGA 420
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Db 721 AGAG 724

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LOCUS CQ727837 680 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 13771 from Patent WO02068579.
ACCESSION CQ727837
VERSION CQ727837.1 GI:42294978
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 13771 06-SEP-2002;
PE Corporation (NY) (US)
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Best Local Similarity 100.0%; Pred. No. 2.2e-152;
Matches 680; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 13
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DEFINITION Mus musculus expressed sequence AA536743, mRNA (cdna clone
BC066137
ACCESSION BC066137
VERSION BC066137.1 GI:42490934
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Murinae; Mus.
1 (bases 1 to 2481)
Strausberg RH, Feilgold EA, Grouse LH, Derge JG, Klausner RD,
Collins FS, Wagner L, Sherman CM, Schuler GD, Altschul SF, Zeeberg
B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
GM, Hong L, Stapleton M, Soares MB, Bonaldo MP, Casavant TL,
Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullaly
SJ, Bosak SH, McEwan FJ, McKernan KJ, Malek JA, Gunaratne PH,
Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,
Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahy J,
Helton E, Kettelman M, Madan A, Rodrigues S, Sanchez A, Whiting M,
Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
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CONSRM
TITLE

JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Snaillus DE, Schmerch A, Schein JE, Jones SJ and Marra MA.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 2481)
Director MGC Project.
Submitted (03-FEB-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Minoru Ko
cDNA Library Preparation: Yulan Piao and Minoru Ko (National
Institute on Aging, NIH: http://lgsun.grc.nia.nih.gov/cDNA//)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 144 Row: a Column: 18.

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Matches 738; Conservative 0; Mismatches 174; Indels 3; Gaps 1;
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RESULT 14
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LOCUS
DEFINITION
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ACCESSION
BC066160
VERSION
BC066160.1 GI:42490882
KEYWORDS
MGC.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 2481)
Straussberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,

Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
GM, Hong L, Stapleton M, Soares MB, Bonaldo MP, Casavant TL,
Schetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P,
Prange C, Raha SS, Loquellano NA, Peters GU, Abramson RD, Mullahy
SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,
Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyak SW,
Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
Helton E, Kettman M, Madan A, Rodriguez S, Sanchez A, Whiting M,
Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakeley RW,
Touhman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
Schmutz J, Myers RM, Butterfield YS, Krzywiecki MI, Skalska U,
Smalusz DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2481)
Director MGC Project.
Direct Submission
Submitted (03-FEB-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NTH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gcgpc@remail.nih.gov
Tissue Procurement: Minoru Ko
cDNA Library Preparation: Yulan Piao and Minoru Ko (National
Institute on Aging, NIH: http://lgaun.grc.nia.nih.gov/cDNA/)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 144 Row: a Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 22122334.

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VTKVEHKSQKERRSLMSVSGIESVNGDVPATPVKRRSRDTE"

gene

CDS

ORIGIN

Query Match 48.1%; Score 520.6; DB 9; Length 2481;
Best Local Similarity 80.7%; Pred. No. 4.7e-138;
Matches 738; Conservative 0; Mismatches 174; Indels 3; Gaps 1;

QY 14 CCGCCGCTCCGAGCGGCTCTCCCTTCCGAGCGGGACGCGGCCCTGGGGGAGG 73
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RESULT 15

AC027607/c

LOCUS

DEFINITION Homo sapiens BAC clone RP11-36B15 from 4, complete sequence.

161070 bp DNA linear

AC027607

LOCUS

DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISMAC027607
AC027607.7 GI:21686941
HTG.

Homo sapiens

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED1 (bases 1 to 161070)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
9847074REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED2 (bases 1 to 161070)
Cordes, M., Cotton, M., Bradshaw-Cordum, H. and Boyer, E.
The sequence of Homo sapiens BAC clone RP11-36B15
Unpublished (2001)REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED3 (bases 1 to 161070)
Waterston, R.H.
Direct Submission
Submitted (30-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USAREFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED4 (bases 1 to 161070)
Waterston, R.
Direct Submission
Submitted (03-JUL-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jul 3, 2002 this sequence version replaced gi:15321552.REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMEDCenter: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@watson.wustl.edu
----- Summary Statistics -----
Center project name: H_NH0036B15

COMMENT

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong
and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-562N2, 2000 bp overlap; the
clone sequenced to the right is RP11-9D8, 2000 bp overlap. Actual
start of this clone is at base position 1 of RP11-36B15; actual end
is at base position 161070 of RP11-36B15.

Qy	998	TAGGAATGGTATTTGACAGGGAAGTGGGAGAGCTTTCCTTGACCCAGGAAGACTGAGGGG	1057
Db	117230	TAGGAATGGTATTTGACAGGGAAGTGGGAGAGCTTTCCTTGACCCAGGAAGACTGAGGGG	117171
Qy	1058	GACTGAACATGATTACTTTGTCTGCCTAGAGCTTCTTTGTAAGAAGTCACAAACTTAGTGC	1117
Db	117170	GACTGAACATGATTACTTTGTCTGCCTAGAGCTTCTTTGTAAGAAGTCACAAACTTAGTGC	117111
Qy	1118	CTCCAGGGGCTTGGCCTGTGTGATAATCAGGATAGAGGATTACTTTGTGAGGCAATGTGGC	1177
Db	117110	CTCCAGGGGCTTGGCCTGTGTGATAATCAGGATAGAGGATTACTTTGTGAGGCAATGTGGC	117051
Qy	1178	ATGGTGGGGATTGTGGCAAACTAGNAATTCAATCACCCACCATTATAGGGCTTGCAATACC	1237
Db	117050	ATGGTGGGGATTGTGGCAAACTAGNAATTCAATCACCCACCATTATAGGGCTTGCAATACC	116991
Qy	1238	ACGAGGCAGAAAGCACCTAGTGTGCTGCTCTTCTTACGCAAAAAA	1291
Db	116990	ACGAGGCAGAAAGCACCTAGTGTGCTGCTCTTCTTACGCAAAAAA	116937

Search completed: February 23, 2006, 17:05:11
Job time : 6923 secs

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PR 06-JUN-1997; 97US-0048877P.
PR 06-JUN-1997; 97US-0048878P.
PR 06-JUN-1997; 97US-0048880P.
PR 06-JUN-1997; 97US-0048881P.
PR 06-JUN-1997; 97US-0048882P.
PR 06-JUN-1997; 97US-0048883P.
PR 06-JUN-1997; 97US-0048884P.
PR 06-JUN-1997; 97US-0048885P.
PR 06-JUN-1997; 97US-0048889P.
PR 06-JUN-1997; 97US-0048892P.
PR 06-JUN-1997; 97US-0048893P.
PR 06-JUN-1997; 97US-0048894P.
PR 06-JUN-1997; 97US-0048895P.
PR 06-JUN-1997; 97US-0048896P.
PR 06-JUN-1997; 97US-0048897P.
PR 06-JUN-1997; 97US-0048898P.
PR 06-JUN-1997; 97US-0048899P.
PR 06-JUN-1997; 97US-0048900P.
PR 06-JUN-1997; 97US-0048901P.
PR 06-JUN-1997; 97US-0048915P.
PR 06-JUN-1997; 97US-0048916P.
PR 06-JUN-1997; 97US-0048917P.
PR 06-JUN-1997; 97US-0048949P.
PR 06-JUN-1997; 97US-0048962P.
PR 06-JUN-1997; 97US-0048963P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048970P.
PR 06-JUN-1997; 97US-0048971P.
PR 06-JUN-1997; 97US-0048972P.
PR 06-JUN-1997; 97US-0049019P.
PR 06-JUN-1997; 97US-0049020P.
PR 06-JUN-1997; 97US-0049373P.
PR 06-JUN-1997; 97US-0049374P.
PR 06-JUN-1997; 97US-0049375P.
PR 05-SEP-1997; 97US-0057584P.
PR 05-SEP-1997; 97US-0057627P.
PR 05-SEP-1997; 97US-0057628P.
PR 05-SEP-1997; 97US-0057629P.
PR 05-SEP-1997; 97US-0057634P.
PR 05-SEP-1997; 97US-0057635P.
PR 05-SEP-1997; 97US-0057642P.
PR 05-SEP-1997; 97US-0057643P.
PR 05-SEP-1997; 97US-0057644P.
PR 05-SEP-1997; 97US-0057645P.
PR 05-SEP-1997; 97US-0057646P.
PR 05-SEP-1997; 97US-0057647P.
PR 05-SEP-1997; 97US-0057648P.
PR 05-SEP-1997; 97US-0057649P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057651P.
PR 05-SEP-1997; 97US-0057654P.
PR 05-SEP-1997; 97US-0057661P.
PR 05-SEP-1997; 97US-0057662P.
PR 05-SEP-1997; 97US-0057666P.
PR 05-SEP-1997; 97US-0057667P.
PR 05-SEP-1997; 97US-0057668P.
PR 05-SEP-1997; 97US-0057760P.
PR 05-SEP-1997; 97US-0057761P.
PR 05-SEP-1997; 97US-0057762P.
PR 05-SEP-1997; 97US-0057763P.
PR 05-SEP-1997; 97US-0057764P.
PR 05-SEP-1997; 97US-0057765P.
PR 05-SEP-1997; 97US-0057769P.
PR 05-SEP-1997; 97US-0057770P.
PR 05-SEP-1997; 97US-0057771P.
PR 05-SEP-1997; 97US-0057774P.
PR 05-SEP-1997; 97US-0057775P.
PR 05-SEP-1997; 97US-0057776P.
PR 05-SEP-1997; 97US-0057777P.
PR 05-SEP-1997; 97US-0057778P.
PR 18-DEC-1997; 97US-0070923P.
XX PA (HUMA-) HUMAN GENOME SCI INC.

XX Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Hu J;
PI Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C;
PI Florence K, Lafleur DW, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR;
PI Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA,
PI Carter KC;
XX WPI; 1999-059865/05.
DR P-PSDB; AAW88579.
XX New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX Claim 4; Page 315-316; 772pp; English.
XX The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
CC encoding human secreted proteins (AAW88534 to AAW88756). The secreted
CC protein gene sequences are deposited with the ATCC under deposit numbers
CC ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
CC cells comprising recombinant vectors containing the nucleic acid
CC sequences are used for the recombinant production of the secreted
CC proteins. The polynucleotide and amino acid sequences are useful for are
CC useful for preventing, treating or ameliorating medical conditions e.g.
CC by protein or gene therapy. Pathological conditions can be also diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the polynucleotides, based on
CC which tissues they are most highly expressed in, and include developing
CC products for the diagnosis or treatment of cancer, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC retinosis, prostate diseases, obesity, disorders involving osteoclasts
CC such as osteoporosis, arthritis or malignancies, diseases of testes, lung
CC or thymus, digestive/endocrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners. The
CC present sequence represents a gene encoding a human secreted protein (see
CC descriptor line for gene number and clone identification)
XX SQ Sequence 1603 BP; 416 A; 356 C; 449 G; 371 T; 0 U; 11 Other;

Query Match 92.7%; Score 1196.6; DB 2; Length 1603;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1268; Conservative 5; Mismatches 13; Indels 9; Gaps 6;

Qy 1 CCCACGGCTCCGGCCCGCCCGGCTCCGAGCGGCTCTCCCTTCCGAGCGCGGAGCGGC 60
Db 7 CCCACGGCTCCGGCCCGCCCGGCTCCGAGCGGCTCTCCCTTCCGAGCGCGGAGCGGC 64

Qy 61 GCCCTGGGGAGGAGGGGGAGCGACCGGGGATGGCTCCGGCGGCACTCCGGGGTCCG 120
Db 65 GCCCTGGGGAGGAGGGGGAGCGAA-CGACCGGGCGATGGCTCCGGCGGCACTCCGGGGTCCG 123

Qy 121 CCGTCTTAGCGCTGCTGTCTTCTGTGGAGCGCGCTGAGTTCGCGCTGGTCCGG 180
Db 124 CCGTCTTAGCGCTGCTGTCTTCTGTGGAGCGCGCTGAGTTCGCGCTGGTCCGG 183

Qy 181 ACAATGGGAGCAGCCGACATTTGCACTCCAGAAACAGAGACGACCCGTCGCCAGCAACG 240
Db 184 ACAATGGGAGCAGCCGACATTTGCACTCCAGAAACAGAGACGACCCGTCGCCAGCAACG 243

Qy 241 ATACTGGGAATGGACACCCAGAAATATATTTGATACAGCGCTTGTCTGTCTTTATCA 300
Db 244 ATACTGGGAATGGACACCCAGAAATATATTTGATACAGCGCTTGTCTGTCTTTATCA 303

Qy 301 TGGGTCTTTTGGCGTCTCTATTTGCCACCTGC---TTAAGAAAGAAAGGCTATCGTTGTA 357
Db 304 TGGGTCTTTTGGCGTCTCTATTTGCCACCTGC---TTAAGAAAGAAAGGCTATCGTTGTA 363

Qy 358 CAACAGAAAGCAGCAAGATATCGAAGAGG-AAAGGTTGAAAGATAGATTAATGAATGAC 416
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Qy 61 GCCGTGGGGAGGAGGGCGAAGCGACCGCGCGATGGCTCCGCGGGCACTCCCGGGGTCCG 120
Db 65 GCCGTGGGGAGGAGGGCGAAGCGACCGCGCGATGGCTCCGCGGGCACTCCCGGGGTCCG 123
Qy 121 CCGTCTAGCGCTGCTGCTCTTCGTGGAGCGCGCGTGGTTCGCGCGTGGTCTCGG 180
Db 124 CCGTCTAGCGCTGCTGCTCTTCGTGGAGCGCGCGTGGTTCGCGCGTGGTCTCGG 183
Qy 181 ACAAATGGGAGCAGCCGCACTATGCACTCCAGAAACAGAGACGACCCCGTCCGCCAGCAACG 240
Db 184 ACAAATGGGAGCAGCCGCACTATGCACTCCAGAAACAGAGACGACCCCGTCCGCCAGCAACG 243
Qy 241 ATACTGGGAATGGACACCCAGAAATATATGTCATACGCGCTTGTCCCTGTGTTCTTTATCA 300
Db 244 ATACTGGGAATGGACACCCAGAAATATATGTCATACGCGCTTGTCCCTGTGTTCTTTATCA 303
Qy 301 TGGGTCTCTTTGGCGTCTCTCAATTTGCCACCTGC---TTAAGAAGAAAGGCTATCGTTGTA 357
Db 304 TGGGTCTCTTTGGCGTCTCTCAATTTGCCACCTGC---TTAAGAAGAAAGGCTATCGTTGTA 363
Qy 358 CAACAGAGCAGACAGATATCGAAGAGG-AAAAGGTTGAAAAGATAGAAATTTGAATGAC 416
Db 364 CAACAGAGCAGACAGATATCGAAGAGAAAGGTTGAAAGWTAGRAATTTGAATGAC 423
Qy 417 AGTGTGAATGAAACAGTGACACTGTTGGGCAAAATCGTCCATCATCATGAAATAATGAA 476
Db 424 AGTGTGAATGAAACAGTGACACTGTTGGGCAAAATCGTCCATCATCATGAAATAATGAA 483
Qy 477 GCGAATCTGATGCTTTAAAGGCGATGTTAGCAGATTAACAGCTGTATGATCTCTGAAGC 536
Db 484 GCGAATCTGATGCTTTAAAGGCGATGTTAGCAGATTAACAGCTGTATGATCTCTGAAGC 543
Qy 537 CCCGTGACCCCCAGCACACAGGAGCGCCGACGTAGTCTCGGCGCTTTGTACACAGGG 596
Db 544 CCCGTGACCCCCAGCACACAGGAGCGCCGACGTAGTCTCGG-CTTTGTACACAGGG 602
Qy 597 GGGACGCCAGGAAAGCAGTCTGTGGCCATCATCTGCATACGTTGGCGGCTGTTGTGAG 656
Db 603 GGGACGCCAGGAAAGCAGTCTGTGGCCATCATCTGCATACGTTGGCGGCTGTTGTGAG 662
Qy 657 AGGGATGTGTCTATCGGTGTAGGCACAGCGGTGCGACATTTATAAGCCCACTAAACAAG 716
Db 663 AGGGATGTGTCTATCGGTGTAGGCACAGCGGTGCGACATTTATAAGCCCACTAAACAAG 722
Qy 717 TCCAGAGAGCAGCACACCGCGCCAAAGCGGAGGTACGGTCTCTTCTGTTGGCAGATTT 776
Db 723 TCCAGAGAGCAGCACACCGCGCCAAAGCGGAGGTACGGTCTCTTCTGTTGGCAGATTT 782
Qy 777 AGAGTTACAAAGTGGAGCACAACTCAAAACAGAAAGAAACCGGAGCCCTGATCTGTT 836
Db 783 AGAGTTACAAAGTGGAGCACAACTCAAAACAGAAAGAAACCGGAGCCCTGATCTGTT 842
Qy 837 AGTGGGCTGAAACCGTCAATGGGAGGTGCGGCAACACCTGTGAAGAGAACCGAGT 896
Db 843 AGTGGGCTGAAACCGTCAATGGGAGGTGCGGCAACACCTGTGAAGAGAACCGAGT 902
Qy 897 GGACACAGTAGCAGGTGAGCCGTGTTTGGTGCACATTTGGGGCAGAGTGGTGCAGGT 956
Db 903 GGACACAGTAGCAGGTGAGCCGTGTTTGGTGCACATTTGGGGCAGAGTGGTGCAGGT 962
Qy 957 GAGGAGAGGTACTTTGGAGCCTCCAGGTGCTGGCAGCATAGGAATGGTATTGACAG 1016
Db 963 GAGGAGAGGTACTTTGGAGCCTCCAGGTGCTGGCAGCATAGGAATGGTATTGACAG 1022
Qy 1017 GGAAGTGGGAGAGCTTTGTTGACCCAGGAAGACTGAGGGGACTGAAACATGATTACTTG 1076
Db 1023 GGAAGTGGGAGAGCTTTGTTGACCCAGGAAGACTGAGGGGACTGAAACATGATTACTTG 1082
Qy 1077 TCTCCCTAGAGCTTTCTGTTAAAGAGTACAAAATTTAGTGCCTCCAGGGCTTCGCTGT 1136
Db 1083 TCTCCCTAGAGCTTTCTGTTAAAGAGTACAAAATTTAGTGCCTCCAGGGCTTCG-CTGT 1141
Qy 1137 GTGATAATGAGGATAGAGGATTACTTTGTGAGGCAATGTGGCATGTGGGATTTGTGGCAA 1196

Db 1142 GTGATAATGAGGATAGAGGATTACTTTGTGAGGCAATGTGGCATGTGGGATTTGGCAA 1201
Qy 1197 ACTAGAATTACATCACCCACCATATAGGGCTTGCAATTACCACGAGGCAGAAAGCACCTA 1256
Db 1202 ACTAGAATTACATCACCCACCATATAGGGCTTGCAATTACCACGAGGCAGAAAGCACCTA 1261
Qy 1257 GTGTGTGTCATCTTTTACGCAAAAAA 1291
Db 1262 GTGTGTGTCATCTTTTACGCAAAAAAAGACAAA 1296

RESULT 4.
ACH04740
ID ACH04740 standard; cDNA; 1603 BP.
XX ACH04740;
XX AC ACH04740;
XX AC ACH04740;
XX 02-OCT-2003 (first entry)
XX Novel human secreted protein #46 cDNA.
DE Human; ss; gene therapy; autoimmune disorder; multiple sclerosis; cancer;
KW systemic lupus erythematosus; haematopoietic cell disorder; allergy;
KW agammaglobulinaemia; ataxia telangiectasia; blood coagulation disorder;
KW afibrinogenemia; thrombocytopenia; graft-versus-host disease; arthritis;
KW inflammatory condition; ischaemia-reperfusion injury; infectious disease;
KW hyperproliferative disorder; purpura; viral infection; regeneration;
KW bacterial infection; ulcer; Alzheimer's disease; gene.
XX OS Homo sapiens.
XX US2003065160-A1.
XX 03-APR-2003.
XX 07-DEC-2001; 2001US-00004860.
PR 06-JUN-1997; 97US-0048875P.
PR 06-JUN-1997; 97US-0048876P.
PR 06-JUN-1997; 97US-0048877P.
PR 06-JUN-1997; 97US-0048878P.
PR 06-JUN-1997; 97US-0048880P.
PR 06-JUN-1997; 97US-0048881P.
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PR 06-JUN-1997; 97US-0048883P.
PR 06-JUN-1997; 97US-0048884P.
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PR 06-JUN-1997; 97US-0048892P.
PR 06-JUN-1997; 97US-0048893P.
PR 06-JUN-1997; 97US-0048894P.
PR 06-JUN-1997; 97US-0048895P.
PR 06-JUN-1997; 97US-0048896P.
PR 06-JUN-1997; 97US-0048897P.
PR 06-JUN-1997; 97US-0048898P.
PR 06-JUN-1997; 97US-0048899P.
PR 06-JUN-1997; 97US-0048900P.
PR 06-JUN-1997; 97US-0048901P.
PR 06-JUN-1997; 97US-0048915P.
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PR 06-JUN-1997; 97US-0048971P.
PR 06-JUN-1997; 97US-0048972P.
PR 06-JUN-1997; 97US-0048974P.
PR 06-JUN-1997; 97US-0049019P.
PR 06-JUN-1997; 97US-0049020P.
PR 06-JUN-1997; 97US-0049373P.
PR 06-JUN-1997; 97US-0049374P.

PR 06-JUN-1997; 97US-0049375P.
PR 05-SEP-1997; 97US-0057584P.
PR 05-SEP-1997; 97US-0057627P.
PR 05-SEP-1997; 97US-0057628P.
PR 05-SEP-1997; 97US-0057629P.
PR 05-SEP-1997; 97US-0057634P.
PR 05-SEP-1997; 97US-0057635P.
PR 05-SEP-1997; 97US-0057642P.
PR 05-SEP-1997; 97US-0057643P.
PR 05-SEP-1997; 97US-0057644P.
PR 05-SEP-1997; 97US-0057645P.
PR 05-SEP-1997; 97US-0057646P.
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PR 05-SEP-1997; 97US-0057648P.
PR 05-SEP-1997; 97US-0057649P.
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PR 05-SEP-1997; 97US-0057667P.
PR 05-SEP-1997; 97US-0057668P.
PR 05-SEP-1997; 97US-0057760P.
PR 05-SEP-1997; 97US-0057761P.
PR 05-SEP-1997; 97US-0057762P.
PR 05-SEP-1997; 97US-0057763P.
PR 05-SEP-1997; 97US-0057764P.
PR 05-SEP-1997; 97US-0057765P.
PR 05-SEP-1997; 97US-0057769P.
PR 05-SEP-1997; 97US-0057770P.
PR 05-SEP-1997; 97US-0057771P.
PR 05-SEP-1997; 97US-0057774P.
PR 05-SEP-1997; 97US-0057775P.
PR 05-SEP-1997; 97US-0057776P.
PR 05-SEP-1997; 97US-0057777P.
PR 05-SEP-1997; 97US-0057778P.
PR 05-SEP-1997; 97US-0070923P.
PR 04-JUN-1998; 98WO-US011422.
PR 15-JUL-1998; 98US-0092921P.
PR 30-JUL-1998; 98US-0094657P.
PR 04-DEC-1998; 98US-0020525P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Young P, Greene JM, Ruben SM, Rosen CA, Hu J;
PI Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C;
PI Florence K, Lafleur DW, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR;
PI Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA,
PI Carter KC;
DR WFI; 2003-540804/51.
DR P-PSDB; ABO44603.
XX
XX New isolated protein, useful for preparing a composition for diagnosing
PT or treating cancer, inflammatory, immune or infectious diseases.
PS Example 1; SEQ ID NO 56; 172pp; English.
XX
CC The invention relates to an isolated HEMAB80 protein. The protein is
CC useful for preparing a composition for diagnosing or treating autoimmune
CC disorders e.g. multiple sclerosis and systemic lupus erythematosus;
CC haematopoietic cell disorders e.g. agammaglobulinaemia and ataxia
CC triangiectasia; blood coagulation disorders e.g. afibrinogenemia and
CC thrombocytopenia; allergy; graft-versus-host disease; inflammatory
CC conditions e.g. ischaemia-reperfusion injury and arthritis;
CC hyperproliferative disorders e.g. cancer and purpura; infectious disease
CC e.g. viral infection and bacterial infection. The polynucleotide or
CC protein can be used to regenerate damaged tissue e.g. ulcers and
CC Alzheimer's disease. The present sequence represents a novel human
CC secreted protein cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?DocID=20030065160
XX
SQ Sequence 1603 BP; 416 A; 356 C; 449 G; 371 T; 0 U; 11 Other;
Query Match 92.7%; Score 1196.6; DB 9; Length 1603;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1268; Conservative 5; Mismatches 13; Indels 9; Gaps 6;
Qy 1 CCACGCGTCCGGCCCGCGCTCCGGAGCGGCTCTGCCCTCCGAGCGGCGGAGCGGCG 60
Db 7 CCCACGCGTCCGGCCCGCGCTCCGGAGCGGCTCTGCCCTCCGAGCGGCGGAG--CCGC 64
Qy 61 GCCTGGGGGAGAGGCGGAGCGAGCGGCGGATGGCTCCGCGGCACTCCCGGGTCCG 120
Db 65 GCGCTGGGGGAGAGGCGGAG--CGACGCGGCGATGGCTCCGCGGCACTCCCGGGTCCG 123
Qy 121 CCGTCTAGCGCGTGTCTCTTGGGAGCGCGGTGAGTTGGCCCTGGTGGCTCCGG 180
Db 124 CCGTCTAGCGCGTGTCTTCTTGGGAGCGCGGTGAGTTGGCGCTGGTGGCTCCGG 183
Qy 181 ACAATGGGAGCGCGCACATTGCACTCCAGAACAGAGACGACCCCTCGCCCAAGACG 240
Db 184 ACAATGGGAGCGCGCACATTGCACTCCAGAACAGAGACGACCCCTCGCCCAAGACG 243
Qy 241 ATACTGGGAATGACACCCAGAAATATATTCATACGCGCTTGTCCCTGTGTTTATCA 300
Db 244 ATACTGGGAATGACACCCAGAAATATATTCATACGCGCTTGTCCCTGTGTTTATCA 303
Qy 301 TGGGTCTCTTTGGCGTCTCATTTGCCACCTGC---TTAAGAGAAAGAGGTATCGTTGTA 357
Db 304 TGGGTCTCTTTGGCGTCTCATTTNGCCAMCTNGCTTNAAGAGAAAGGTATCGTTGTA 363
Qy 358 CAACAGAGCAGAGCAAGATATCGAAGAGG-AAAAGTTGAAAGATAGAAATGAATGAC 416
Db 364 CAACAGAGCAGAGCAAGATATCGAAGAGAAAGGTTGAAAGWTAGRATTGAATGAC 423
Qy 417 AGTGTGAATGAACAGAGTGCACCTGTTGGCAATCGTCCACTACATACATGAAATGAA 476
Db 424 AGTGTGAATGAACAGAGTGCACCTGTTGGCAATCGTCCACTACATGAAATGAA 483
Qy 477 GCGAATGCTGATGCTTTAAAGGCGATGGTAGCAGATAACAGCCCTGTATGATTCCTGAAAGC 536
Db 484 GCGAATGCTGATGCTTTAAAGGCGATGGTAGCAGATAACAGCCCTGTATGATTCCTGAAAGC 543
Qy 537 CCGTGACCCCGCAGACACACAGGAGCGCCCGCAGTAGTGCTCGGCCCTTTGTACACAGG 596
Db 544 CCGTGACCCCGCAGACACACAGGAGCGCCCGCAGTAGTGCTCGGG-CTTTGTACACAGG 602
Qy 597 GGGACGCCAGGAAGCAGCTCTGTGGCCATCATCTGCATACGGTGGGCGGTGTTGTCGAG 656
Db 603 GGGACGCCAGGAAGCAGCTCTGTGGCCATCATCTGCATACGGTGGGCGGTGTTGTCGAG 662
Qy 657 AGGATGTGTGTCATCGGTAGGCACAAAGCGGTGGCACTTTTATAAGCCCACTAAACAAG 716
Db 663 AGGATGTGTGTCATCGGTAGGCACAAAGCGGTGGCACTTTTATAAGCCCACTAAACAAG 722
Qy 717 TCAGAGAGAGCAGACCAACCGCCCAAGGCGGAGGTACCGTCTCTTCTGTGGCAGATTT 776
Db 723 TCAGAGAGAGCAGACCAACCGCCCAAGGCGGAGGTACCGTCTCTTCTGTGGCAGATTT 782
Qy 777 AGAGTTACAAAGTGGAGCACAAGTCAAAACAGAGGAACGGAGAGCCCTGATGTCGT 836
Db 783 AGAGTTACAAAGTGGAGCACAAGTCAAAACAGAGGAACGGAGAGCCCTGATGTCGT 842
Qy 837 AGTGGGCGCTGAAACCGTCAATGGGAGGTGCGCGCAACACCTGTGAAGAGAGAACGCGAGT 896
Db 843 AGTGGGCGTGAACCGTCAATGGGAGGTGCGCGCAACACCTGTGAAGAGAGAACGCGAGT 902
Qy 897 GGCAAGAGTAGCAGGTGAGCCCGTGTGTTGGTGACATTTGGGGGAGAGAGTGGTGACGGGT 956
Db 903 GGCAAGAGTAGCAGGTGAGCCCGTGTGTTGGTGACATTTGGGGGAGAGAGTGGTGACGGGT 962
Qy 957 GAGGAGAGAGTACTTTGGAGGCTCCCGAGGCTGTGTGGCAGCATAGGAATGGTATTGACAG 1016

Db 963 GAGGAGAGGACCTGGAGCCTCCAGGTGCTGGCAGCATAGGAATGGTAATTGACAG 1022
Qy 1017 GGAAGTGGGAGAGCTTTCTTTGACCCAGGAAGACTGAGGGGAGCTGAACATGATTACTTGG 1076
Db 1023 GGAAGTGGGAGAGCTTTCTTTGACCCAGGAAGACTGAGGGGAGCTGAACATGATTACTTGG 1082
Qy 1077 TCTGCTAGAGCTTCTTTGTAAGAAGTCAAACTTAGTGCTCCAGGGGCTTGGCCTGT 1136
Db 1083 TCTGCTAGAGCTTCTTTGTAAGAAGTCAAACTTAGTGCTCCAGGGGCTTGG-CTGT 1141
Qy 1137 GTGATAATGAGATAGAGGATTACTTGTGAGGCAATGGCATGGTGGGATTTGGCAA 1196
Db 1142 GTGATAATGAGATAGAGGATTACTTGTGAGGCAATGGCATGGTGGGATTTGGCAA 1201
Qy 1197 ACTAGAATTACATCAACCCACCATATAGGCTTGCATTACCGAGGCGAGAAAGCACCCTA 1256
Db 1202 ACTAGAATTACATCAACCCACCATATAGGCTTGCATTACCGAGGCGAGAAAGCACCCTA 1261
Qy 1257 GTGTGTGCTGATCTTCTTACGCAAAAAA 1291
Db 1262 GTGTGTGCTGATCTTCTTACGCAAAAAA 1296

RESULT 5

ID ACD44550
ACD44550 standard; cDNA; 1603 BP.

AC ACD44550;

XX 10-SEP-2003 (first entry)

XX Human cDNA from novel secreted protein gene 46.

XX Human; ss; gene; secreted protein; precerebellin-like protein;
KW neurodegenerative disorder; Huntington's disease; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; schizophrenia; mania;
KW dementia; paranoia; psychosis; autism; immune disorder; infection;
KW inflammation; allergy; liver disorder; hepatoblastoma; jaundice;
KW hepatitis; immunological disorder; AIDS; leukaemia; rheumatoid arthritis;
KW sepsis; acne; psoriasis; cancer.

XX Homo sapiens.

XX US6525174-B1.

XX 25-FEB-2003.

XX 04-DEC-1998; 98US-00205258.

XX 06-JUN-1997; 97US-0048875P.

XX 06-JUN-1997; 97US-0048876P.

XX 06-JUN-1997; 97US-0048877P.

XX 06-JUN-1997; 97US-0048878P.

XX 06-JUN-1997; 97US-0048880P.

XX 06-JUN-1997; 97US-0048881P.

XX 06-JUN-1997; 97US-0048882P.

XX 06-JUN-1997; 97US-0048883P.

XX 06-JUN-1997; 97US-0048884P.

XX 06-JUN-1997; 97US-0048885P.

XX 06-JUN-1997; 97US-0048886P.

XX 06-JUN-1997; 97US-0048887P.

XX 06-JUN-1997; 97US-0048888P.

XX 06-JUN-1997; 97US-0048889P.

XX 06-JUN-1997; 97US-0048890P.

XX 06-JUN-1997; 97US-0048891P.

XX 06-JUN-1997; 97US-00488915P.

XX 06-JUN-1997; 97US-00488916P.

XX 06-JUN-1997; 97US-00488917P.

PR 06-JUN-1997; 97US-0048949P.
PR 06-JUN-1997; 97US-0048962P.
PR 06-JUN-1997; 97US-0048963P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048970P.
PR 06-JUN-1997; 97US-0048971P.
PR 06-JUN-1997; 97US-0048972P.
PR 06-JUN-1997; 97US-0048974P.
PR 06-JUN-1997; 97US-0049019P.
PR 06-JUN-1997; 97US-0049020P.
PR 06-JUN-1997; 97US-0049373P.
PR 06-JUN-1997; 97US-0049374P.
PR 06-JUN-1997; 97US-0049375P.
PR 05-SEP-1997; 97US-0057584P.
PR 05-SEP-1997; 97US-0057627P.
PR 05-SEP-1997; 97US-0057628P.
PR 05-SEP-1997; 97US-0057629P.
PR 05-SEP-1997; 97US-0057634P.
PR 05-SEP-1997; 97US-0057635P.
PR 05-SEP-1997; 97US-0057642P.
PR 05-SEP-1997; 97US-0057643P.
PR 05-SEP-1997; 97US-0057644P.
PR 05-SEP-1997; 97US-0057645P.
PR 05-SEP-1997; 97US-0057646P.
PR 05-SEP-1997; 97US-0057647P.
PR 05-SEP-1997; 97US-0057648P.
PR 05-SEP-1997; 97US-0057649P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057651P.
PR 05-SEP-1997; 97US-0057654P.
PR 05-SEP-1997; 97US-0057661P.
PR 05-SEP-1997; 97US-0057662P.
PR 05-SEP-1997; 97US-0057666P.
PR 05-SEP-1997; 97US-0057667P.
PR 05-SEP-1997; 97US-0057668P.
PR 05-SEP-1997; 97US-0057760P.
PR 05-SEP-1997; 97US-0057761P.
PR 05-SEP-1997; 97US-0057762P.
PR 05-SEP-1997; 97US-0057763P.
PR 05-SEP-1997; 97US-0057764P.
PR 05-SEP-1997; 97US-0057765P.
PR 05-SEP-1997; 97US-0057766P.
PR 05-SEP-1997; 97US-0057767P.
PR 05-SEP-1997; 97US-0057768P.
PR 18-DEC-1997; 97US-0070923P.
PR 04-JUN-1998; 98WO-US011422.
PR 15-JUL-1998; 98US-0092921P.
PR 30-JUL-1998; 98US-0094657P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.

XX Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Hu J;
XX Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C;
XX Florence K, Lafleur DW, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR;
XX Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA;
XX Carter KC;

XX MPI: 2003-511926/48.
XX P-PSDB; ABO26083.

XX New precerebellin-like protein, useful for diagnosing or treating
XX neurodegenerative and behavioral disorders, immune disorders, liver
XX disorders, and cancer.

XX Example 1; SEQ ID NO 56; 156pp; English.

XX The invention relates to an isolated protein comprising amino acid
XX residues 33-205 or 1-205 of a novel human secreted protein appearing as

CC ABO26252. The protein is encoded by one of 238 disclosed cDNA sequences
CC encoding 238 secreted proteins. ABO26252 is a precerebellin-like protein.
CC Also included are a composition comprising the protein and a carrier and
CC an isolated protein produced by expressing the protein cited above by a
CC cell, and recovering the protein. The proteins are useful for diagnosing
CC or treating neurodegenerative and behavioural disorders (e.g. Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, schizophrenia, mania,
CC dementia, paranoia, psychoses or autism), immune disorders (e.g.
CC infection, inflammation, allergy), liver disorders (e.g. hepatoblastoma,
CC jaundice, hepatitis), immunological disorders (e.g. AIDS, leukaemia,
CC rheumatoid arthritis, sepsis, acne, psoriasis) and cancer. The present
CC sequence is one of the 238 disclosed cDNAs encoding a novel secreted
CC protein. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from USPTO at:- seqdata.uspto.gov/sequence.html?docID=6525174B1
XX

SQ Sequence 1603 BP; 416 A; 356 C; 449 G; 371 T; 0 U; 11 Other;

Query Match 92.7%; Score 1196.6; DB 9; Length 1603;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1268; Conservative 5; Mismatches 13; Indels 9; Gaps 6;

Qy	1	CCCAACGGCTCCGGCCCGCCCGCTCCGAGCGGCTCTGCTTCCGAGCGCGGACGCGGC	60
Db	7	CCCAACGGCTCCGGCCCGCCCGCTCCGAGCGGCTCTGCTTCCGAGCGCGGACGCGGC	64
Qy	61	GCCTTGGGGAGGAGGCGGAGCGACCGGGCGATGGCTCCGCGGCGACTCCCGGGGTCCG	120
Db	65	GCCTTGGGGAGGAGGCGGAGCGACCGGGCGATGGCTCCGCGGCGACTCCCGGGGTCCG	123
Qy	121	CCGTCTAGCGCTGCTGCTCTTCTGGGAGCGCGGTGAGTTCCGCGCTGCTGCTCCGG	180
Db	124	CCGTCTAGCGCTGCTGCTCTTCTGGGAGCGCGGTGAGTTCCGCGCTGCTGCTCCGG	183
Qy	181	ACAAATGGGAGCAGCGGCACATTTGACATCCAGAACAGAGACGACCCCGTCCGCCAGCAACG	240
Db	184	ACAAATGGGAGCAGCGGCACATTTGACATCCAGAACAGAGACGACCCCGTCCGCCAGCAACG	243
Qy	241	ATACTGGGAATGACACCCAGAAATATATTTGCATACGGCGTGTGCCCTGTCTTTATCA	300
Db	244	ATACTGGGAATGACACCCAGAAATATATTTGCATACGGCGTGTGCCCTGTCTTTATCA	303
Qy	301	TGGGTCTCTTTGGGCTCTCATTTGCCACCTGC--TTAAGAGAAAGGCTATCGTTGTA	357
Db	304	TGGGTCTCTTTGGGCTCTCATTTNGCCAMCTGCTTNAAGAGAAAGGCTATCGTTGTA	363
Qy	358	CAACAGAGCAGAGCAAGATATCGAAGAGG-AAAAGGTTGAAAAGATAGAAATGAATGAC	416
Db	364	CAACAGAGCAGAGCAAGATATCGAAGAGAAAGGTTGAAAAGATAGAAATGAATGAC	423
Qy	417	AGTGTGAATGAAACAGTGAACACTGTTGGGCAATCGTCCACTACATCATGAAATAAGAA	476
Db	424	AGTGTGAATGAAACAGTGAACACTGTTGGGCAATCGTCCACTACATCATGAAATAAGAA	483
Qy	477	GCGAATGCTGATGCTTTAAAGGCGCATGTAGCAGATAACAGCCTGTATGATCTCTGAAAGC	536
Db	484	GCGAATGCTGATGCTTTAAAGGCGCATGTAGCAGATAACAGCCTGTATGATCTCTGAAAGC	543
Qy	537	CCCGTGACCCCGACACACAGGAGCGCGCAGTGAGTCTCTGGGCGCTTTGTACACAGGG	596
Db	544	CCCGTGACCCCGACACACAGGAGCGCGCAGTGAGTCTCTGGGCGCTTTGTACACAGGG	602
Qy	597	GGAGCGCCAGGAGAGCAGCTGTGTGGGCATCATCTGCATACGCGTGGCGGTGTGTGCGAG	656
Db	603	GGAGCGCCAGGAGAGCAGCTGTGTGGGCATCATCTGCATACGCGTGGCGGTGTGTGCGAG	662
Qy	657	AGGATGTGTGTCATCGGTGTAGGACACAGCGGTGGCACTTTATAAAGCCCACTAAACAAG	716
Db	663	AGGATGTGTGTCATCGGTGTAGGACACAGCGGTGGCACTTTATAAAGCCCACTAAACAAG	722
Qy	717	TCAGAGAGAGCAGACACACCGCGCAGAGGAGGTACGGTCTCTTCTGTGGCAGATTT	776
Db	723	TCAGAGAGAGCAGACACACCGCGCAGAGGAGGTACGGTCTCTTCTGTGGCAGATTT	782

Qy	777	AGAGTTACAAAGCTGGAGCACAACTCAAAACAGAGGAAACGAGAAAGCTGATCTCTGTT	836
Db	783	AGAGTTNACAAAGCTGGAGCACAACTCAAAACAGAGGAAACGAGAAAGCTGATCTCTGTT	842
Qy	837	AGTGGGGCTCAAAACCGCTCAATGGGAGGTGCCGGCAACACCTGTGAAGAGAGAACGAGT	896
Db	843	AGTGGGGCTCAAAACCGCTCAATGGGAGGTGCCGGCAACACCTGTGAAGAGAGAACGAGT	902
Qy	897	GGCACAGAGTAGCAGGTGAGCCGCTGTTGGTGTGACATTTGGGGCAGAGTGGTGCAGGT	956
Db	903	GGCACAGAGTAGCAGGTGAGCCGCTGTTGGTGTGACATTTGGGGCAGAGTGGTGCAGGT	962
Qy	957	GAGGAGAGGTACTTGGAGCGCTCCAGGTCTGTGGCAGCATAGGAATGCTATTGACAG	1016
Db	963	GAGGAGAGGTACTTGGAGCGCTCCAGGTCTGTGGCAGCATAGGAATGCTATTGACAG	1022
Qy	1017	CGAAGTGGGAGAGCTTTCTTTGACCCAGGAAGACTGAGGGGAGCTGAACATGATTACTTG	1076
Db	1023	CGAAGTGGGAGAGCTTTCTTTGACCCAGGAAGACTGAGGGGAGCTGAACATGATTACTTG	1082
Qy	1077	TCTGCCCTAGAGCTTCTTGTAAAGAGTCAAAACTTTAGTGCCTCCAGGGGCTTGGCCTGT	1136
Db	1083	TCTGCCCTAGAGCTTCTTGTAAAGAGTCAAAACTTTAGTGCCTCCAGGGGCTTGG-CTGT	1141
Qy	1137	GTGATATGAGGATAGAGGATTACTTGTGAGGCAATGTGGCATGTTGGGATTTGGGCA	1196
Db	1142	GTGATATGAGGATAGAGGATTACTTGTGAGGCAATGTGGCATGTTGGGATTTGGGCA	1201
Qy	1197	ACTAGAAATTCACATCACCCACCATATAGAGGCTTGCAATACACAGGCGAGAAACACTA	1256
Db	1202	ACTAGAAATTCACATCACCCACCATATAGAGGCTTGCAATACACAGGCGAGAAACACTA	1261
Qy	1257	GTGTGTGTCATCTTCTTACGCAAAAAA 1291	
Db	1262	GTGTGTGTCATCTTCTTACGCAAAAAAAGCAAAA 1296	
RESULT 6			
AAF93833			
ID	AAF93833 standard; cDNA; 1320 BP.		
XX	AAF93833;		
XX	23-MAY-2001 (first entry)		
XX	Human cDNA encoding a membrane or secretory protein clone FSEC0162.		
DE	Human; secretory protein; membrane protein; vaccine; gene therapy;		
KW	rheumatoid arthritis; diabetes; ss.		
OS	Homo sapiens.		
PN	EPI067182-A2.		
XX	10-JAN-2001.		
XX	07-JUL-2000; 2000EP-00114090.		
XX	08-JUL-1999; 99JP-00194179.		
PR	11-JAN-2000; 2000JP-00118775.		
PR	02-MAY-2000; 2000JP-00183766.		
XX	(HELI-) HELIX RES INST.		
XX	Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;		
XX	WPI; 2001-093989/11.		
DR	P-PSDB; AAB88406.		
XX	Nucleic acids encoding secretory proteins/membrane proteins, useful in		
PT	gene therapy or as candidate target molecules in drug development.		

PS Claim 1; SEQ ID NO 179; 609pp + Sequence Listing; English.

XX This invention relates to nucleic acid sequences AAF93744 - AAF93916

CC which encode human secretory or membrane proteins represented by AAB88317

CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and

CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the

CC invention. The invention also includes methods for the production of

CC antibodies directed against the proteins, and cDNA sequences, which can

CC be used in vaccines. The polynucleotide sequences can be used in gene

CC therapy. The polynucleotide sequences and the proteins they encode may be

CC used in the prevention, treatment and diagnosis of diseases associated

CC with inappropriate secretory protein/membrane protein expression. The

CC nucleic acids and complementary sequences may also be used as DNA probes

CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect

CC and quantitate the presence of similar nucleic acid sequences in samples.

CC They may also be used to study the expression and function of secretory

CC proteins/membrane polypeptides and their role in metabolism. The

CC polypeptides may be used as antigens in the production of antibodies

CC against them and in assays to identify modulators (agonists and

CC antagonists) of expression and activity. The antibodies and antagonists

CC may also be used as therapeutic agents to down regulate expression and

CC activity. The antibodies may also be used as diagnostic agents for

CC detecting the presence of the polypeptides in samples (e.g. by enzyme

CC linked immunosorbent assay (ELISA)). Examples of diseases which may be

CC treated include rheumatoid arthritis and diabetes

XX

SQ Sequence 1320 BP; 332 A; 359 C; 370 G; 259 T; 0 U; 0 Other;

Query Match 69.7%; Score 900; DB 5; Length 1320;

Best Local Similarity 99.4%; Pred. No. 4.5e-251;

Matches 903; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ACGGTCGCGGCCCGGCTCCGAGCGGCTCTGCTTCCGAGCGGGACGCGGGGCC 63

DB 1 ACTCGATCAGCCCGCGCTCCGAGCGGCTCTGCTTCCGAGCGGGACGCGGGGCC 60

QY 64 CTGGGGAGGAGGCGGAGCGACGCGCGATGCGTCCGCGGGCACTCCCGGGTCCGCG 123

DB 61 CTGGGGAGGAGGCGGAGCGACGCGCGATGCGTCCGCGGGCACTCCCGGGTCCGCG 120

QY 124 TCCTAGCGCGTCTGCTCTGTTGGAGCGCGGAGTTCGCGCTGCGCTCCGAGCA 183

DB 121 TCCTAGCGCGTCTGCTCTGTTGGAGCGCGGAGTTCGCGCTGCGCTCCGAGCA 180

QY 184 ATGGGAGCAGCGGCACATTGCACTCCAGAACAGAGACGACCCCTCGCCAGCAACGATA 243

DB 181 ATGGGAGCAGCGCGCATTCGACTCCAGAACAGAGACGACCCCTCGCCAGCAACGATA 240

QY 244 CTGGGAATGACACCCAGAAATATATGTCATACGCGCTTGCCTGTCTTTATCATGG 303

DB 241 CTGGGAATGACACCCAGAAATATATGTCATACGCGCTTGCCTGTCTTTATCATGG 300

QY 304 GTCTCTTTGGCGTCTCATTTGCCACCTGCTTAGAGAGAGGCTATCGTTGTACACAG 363

DB 301 GTCTCTTTGGCGTCTCATTTGCCACCTGCTTAGAGAGAGGCTATCGTTGTACACAG 360

QY 364 AAGCAGAGCAGATATCCAGAGGAAAAGTTGAAAAGATAGAAATTCAGTACAGTGTGA 423

DB 361 AAGCAGAGCAGATATCCAGAGGAAAAGTTGAAAAGATAGAAATTCAGTACAGTGTGA 420

QY 424 ATGAAAACAGTGAACATCTGTTGGGCAATTCGTCCTACATCATGAAAATAAGACGAATG 483

DB 421 ATGAAAACAGTGAACATCTGTTGGGCAATTCGTCCTACATCATGAAAATAAGACGAATG 480

QY 484 CTGATGCTTTAAGGCGATGTACAGATACAGCTGTATGATCCTGAAAGCCCCCTGA 543

DB 481 CTGATGCTTTAAGGCGATGTACAGATACAGCTGTATGATCCTGAAAGCCCCCTGA 540

QY 544 CCCCAGCAGACACACGAGCGCCGAGTGTCTCGGCGCTTGTCTACAGGGGGGACGC 603

DB 541 CCCCAGCAGACACACGAGCGCCGAGTGTCTCGGCGCTTGTCTACAGGGGGGACGC 600

QY 604 CAGGGAAGCAGCTCTGTGGCCATCATCTGCATACGGTGGCGGTGTTGTGAGAGGGATG 663

Db 601 CAGGGAAGCAGCTCTGTGGCCATCATCTGCATACGGTGGCGGTGTTGTGAGAGGGATG 660

QY 664 TGTGTCTCGGTGTAGGCACAAGCGGTGGCACTTTTATAAGCCCACTAACCAAGTCCAGAG 723

Db 661 TGTGTCTCGGTGTAGGCACAAGCGGTGGCACTTTTATAAGCCCACTAACCAAGTCCAGAG 720

QY 724 AGAGCAGACACCGCGCCAAAGGCGAGGTCAACGCTCTTCTGTTGGCAGATTTAGAGTTA 783

Db 721 AGAGCAGACACCGCGCCAAAGGCGAGGTCAACGCTCTTCTGTTGGCAGATTTAGAGTTA 780

QY 784 CAAAGTGGAGCACAAGTCAAAACAGAGGAAACGAGAGCGCTGATCTGTTAGTGGG 843

Db 781 CAAAGTGGAGCACAAGTCAAAACAGAGGAAACGAGAGCGCTGATCTGTTAGTGGG 840

QY 844 CTGAAACCGTCAATGGGGAGGTGCGCGCAACACCTGTGAAGAGAGAAACGAGTGGCAGAG 903

Db 841 CTGAAACCGTCAATGGGGAGGTGCGCGCAACACCTGTGAAGAGAGAAACGAGTGGCAGAG 900

QY 904 AGTAGCAG 911

Db 901 AGTAGCAG 908

RESULT 7

ADY63174

ID ADY63174 standard; cDNA; 1320 BP.

XX

AC ADY63174;

XX

DT 02-JUN-2005 (first entry)

XX

DE Human clone PSEC0162 cDNA, SEQ ID 179.

XX

KW Gene therapy; gene; ss.

XX

OS Homo sapiens.

XX

PN EPI514933-A1.

XX

XX 16-MAR-2005.

PD

XX 07-JUL-2000; 2004EP-00027228.

PF

XX 08-JUL-1999; 99JP-00194179.

PR 11-JAN-2000; 2000JP-00118775.

PR 02-MAY-2000; 2000JP-00183766.

PR 07-JUL-2000; 2000EP-00114090.

XX

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX

PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

XX

XX WPI; 2005-203865/22.

DR P-PSDB; ADY63175.

XX

XX Novel isolated polynucleotide encoding human secretory proteins or

PT membrane proteins, useful for examination and diagnosis of abnormality of

PT human secretory proteins.

XX

XX Disclosure; SEQ ID NO 179; 1240pp; English.

PS

XX

CC The present invention relates to novel human secretory proteins or

CC membrane proteins, and their coding sequences. The present sequence is

CC one such coding sequence. The coding sequences of the invention are

CC useful for examination and diagnosis of abnormality of the human

CC secretory proteins and in gene therapy methods. The coding sequences and

CC proteins are useful as candidates for medicines or as target molecules

CC for developing medicines. Antibodies against the proteins of the

CC invention are useful for treating diseases that are associated with the

CC proteins. Note: The sequence data for this patent did not form part of

CC the printed specification, but was obtained from sequence information

CC supplied by the European Patent Office.

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XX
SQ Sequence 1320 BP; 332 A; 359 C; 370 G; 259 T; 0 U; 0 Other;

Query Match      69.7%; Score 900; DB 14; Length 1320;
Best Local Similarity 99.4%; Pred. No. 4.5e-251;
Matches 903; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ACGCGTCCGGCCGCGCGCTCCGAGCGGCTCTGCCCTTCCGAGCGGAGCGGGCGCC 63
DB 1 ACTCGATCAGCCCGCCCGCTCCGAGCGGCTCTGCCCTTCCGAGCGGAGCGGGCGCC 60
QY 64 CTGGGGAGGAGGCGAAGCGACCGCGCATGGCTCCGCGGGCACTCCCGGGGTCCCGCG 123
DB 61 CTGGGGAGGAGGCGAAGCGACCGCGCATGGCTCCGCGGGCACTCCCGGGGTCCCGCG 120
QY 124 TCTTAGCGCTGTCTTCTTCTGTGGGAGCGCGCTGAGTTGCGCGCTGGTGGCTCCGACA 183
DB 121 TCTTAGCGCTGTCTTCTTCTGTGGGAGCGCGCTGAGTTGCGCGCTGGTGGCTCCGACA 180
QY 184 ATGGGAGCAGCGCACATTTGCATCCAGAACAGACGACCCCGTCGCCAGCAACGATA 243
DB 181 ATGGGAGCAGCGCGCATTTGCATCCAGAACAGACGACCCCGTCGCCAGCAACGATA 240
QY 244 CTGGGAATGGACACCCAGAAATATATTGCATACGCGCTTGTCCCTGTGTCTTTATCATGG 303
DB 241 CTGGGAATGGACACCCAGAAATATATTGCATACGCGCTTGTCCCTGTGTCTTTATCATGG 300
QY 304 GTCTCTTTGGCGTCTCATTTGCCACCTGTCTTAAGAAAGAGGCTATCGTTGTACAAAG 363
DB 301 GTCTCTTTGGCGTCTCATTTGCCACCTGTCTTAAGAAAGAGGCTATCGTTGTACAAAG 360
QY 364 AAGCAGAGCAAGATATCGAAGAGGAAAGGTTGAAGAGATAGAAATCAATGACAGTGTGA 423
DB 361 AAGCAGAGCAAGATATCGAAGAGGAAAGGTTGAAGAGATAGAAATCAATGACAGTGTGA 420
QY 424 ATGAAACAGTGCACATGTTGGGCAATCGTCCACTACATCATGAAAAATGAAGCGAATG 483
DB 421 ATGAAACAGTGCACATGTTGGGCAATCGTCCACTACATCATGAAAAATGAAGCGAATG 480
QY 484 CTGATGTCTTAAAGGCGATGGTAGCAGATACAGCCCTGTATGATCTTGAAGGCCCGTGA 543
DB 481 CTGATGTCTTAAAGGCGATGGTAGCAGATACAGCCCTGTATGATCTTGAAGGCCCGTGA 540
QY 544 CCCCAGCACACGAGGAGCCCGCAGTGAGTCTGGGCGCTTGTGTCACGAGGGGAGCG 603
DB 541 CCCCAGCACACGAGGAGCCCGCAGTGAGTCTGGGCGCTTGTGTCACGAGGGGAGCG 600
QY 604 CAGGGAAGCAGCGTCTGTGGCCATCATCTGCATACGCTGGGCGGTGTTGTCGAGAGGGATG 663
DB 601 CAGGGAAGCAGCGTCTGTGGCCATCATCTGCATACGCTGGGCGGTGTTGTCGAGAGGGATG 660
QY 664 TGTGTCATCGGTAGGACACAGCGGTGGCACTTTATAAGCCCACTAAACAAGTCCAGAG 723
DB 661 TGTGTCATCGGTAGGACACAGCGGTGGCACTTTATAAGCCCACTAAACAAGTCCAGAG 720
QY 724 AGAGCAGACACGCGCCAGGCGAGGTACAGGTCCTTTCTGTTGGCAGATTTAGAGTTA 783
DB 721 AGAGCAGACACGCGCCAGGCGAGGTACAGGTCCTTTCTGTTGGCAGATTTAGAGTTA 780
QY 784 CAAAAGTGGAGCACAAGTCAAAACAGAGGAAACGAGAGCCCTGATCTCTGTTAGTGGGG 843
DB 781 CAAAAGTGGAGCACAAGTCAAAACAGAGGAAACGAGAGCCCTGATCTCTGTTAGTGGGG 840
QY 844 CTGAACCGTCAATGGGGAGGTGCGGCAACACTGTTGAAGAGAGAAACGAGTGGCAAG 903
DB 841 CTGAACCGTCAATGGGGAGGTGCGGCAACACTGTTGAAGAGAGAAACGAGTGGCAAG 900
QY 904 AGTAGCAG 911
DB 901 AGTAGCAG 908

AD121815
ID AD121815 standard; cDNA; 1218 BP.
AC AD121815;
XX 15-APR-2004 (first entry)
XX Novel human protein cDNA #74.
XX forensic; nutritional source; damaged tissue; diseased tissue;
XX myeloid cell disorder; lymphoid cell disorder;
XX bone cartilage tissue growth; tendon tissue growth;
XX ligament tissue growth; nerve tissue growth; regeneration; wound healing;
XX tissue repair; tissue replacement; burn; incision; ulcer; cancer; human;
XX ss; gene.
XX Homo sapiens.
OS XX
XX WO2003025148-A2.
XX 27-MAR-2003.
XX 19-SEP-2002; 2002WO-US029964.
XX 19-SEP-2001; 2001US-0323739P.
XX 13-SEP-2002; 2002US-00323739.
XX (HYSB-) HYSEQ INC.
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
XX Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;
XX Haley-Vicente D;
XX WPI; 2003-354603/33.
XX P-PSDB; AD121099.
XX New polynucleotides and secreted proteins, useful for treating myeloid or
XX lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve
XX tissue growth or regeneration, in wound healing, and in tissue repair and
XX replacement.
XX Claim 1; SEQ ID NO 74; 156pp; English.
XX The invention relates to an isolated polynucleotide encoding a
XX polypeptide with biological activity. The polynucleotides and
XX polypeptides are useful in diagnostics, forensics, gene mapping,
XX identification of mutations responsible for genetic disorders and other
XX traits, to assess biodiversity, as nutritional sources or supplements.
XX The polynucleotides may also be used as molecular weight markers,
XX chromosome markers or map related gene positions, or as an antigen to
XX raise anti-DNA antibodies or elicit immune response. The polypeptides are
XX useful for raising antibodies, as markers for tissues in which the
XX corresponding polypeptide is expressed, for re-engineering damaged or
XX diseased tissues, for treating myeloid or lymphoid cell disorders, in
XX bone cartilage, tendon, ligament and/or nerve tissue growth or
XX regeneration, in wound healing, in tissue repair and replacement, in
XX healing of burns, incisions and ulcers, and in treating cancer. The
XX present sequence represents cDNA encoding a novel human protein.
XX
SQ Sequence 1218 BP; 318 A; 302 C; 368 G; 230 T; 0 U; 0 Other;

Query Match      69.0%; Score 891; DB 10; Length 1218;
Best Local Similarity 100.0%; Pred. No. 1.8e-248;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GCTCCGAGCGGCTCTGCTTCCGAGCGGAGCGCGGCGCTTGGGGAGGAGGCGCA 80
DB 1 GCTCCGAGCGGCTCTGCTTCCGAGCGGAGCGCGGCGCTTGGGGAGGAGGCGCA 60
QY 81 AGCGACGCGCGATGGCTCCGCGGGCACTCCCGGGGTCGCCCGCTCTAGCCGCTGTGTC 140
DB 61 AGCGACGCGCGATGGCTCCGCGGGCACTCCCGGGGTCGCCCGCTCTAGCCGCTGTGTC 120
```


Db 542 AGTGAGTCTGGGCTTTGTCCACAGGGGGGACGCCAGGGAAGCACGCTCTGTGGCCATCA 601
Qy 629 TCTGCATACGGTGGGCGTGTTCGAGAGGATGTGTTCATCGGTGTAGGCAACGCG 688
Db 602 TCTGCATACGGTGGGCGTGTTCGAGAGGATGTGTTCATCGGTGTAGGCAACGCG 661
Qy 689 GTGGCACTTTATAAAGCCCACTAACAGTCCAGAGAGAGACACGCGCCCAAGGCGA 748
Db 662 GTGGCACTTTATAAAGCCCACTAACAGTCCAGAGAGAGACACGCGCCCAAGGCGA 721
Qy 749 GGTCAAGCTCTCTCTGTGGCAGATTTAGAGTTACAAAAGTGGAGCACAAGTCAAAACCA 808
Db 722 GGTCAAGCTCTCTCTGTGGCAGATTTAGAGTTACAAAAGTGGAGCACAAGTCAAAACCA 781
Qy 809 GAAGGAACGGGAAGCCCTGATGTCTGTAGTGGGGCTGAACCCGTCATATGGGGAGGTGCC 868
Db 782 CAAGGAACGGGAAGCCCTGATGTCTGTATGGGGCTGAACCCGTCATATGGGGAGGTGCC 841
Qy 869 GGCAACACCTGTGAAGAGA 887
Db 842 GGCAACAACTTGTGAGAGA 860

RESULT 10

AD121359
ID AD121359 standard; cDNA; 861 BP.
XX
AC AD121359;

15-APR-2004 (first entry)

Novel human expressed sequence tag, EST #58.

KW forensic; nutritional source; damaged tissue; diseased tissue;
KW myeloid cell disorder; lymphoid cell disorder;
KW bone cartilage tissue growth; tendon tissue growth;
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human;
KW ss; gene; EST; expressed sequence tag.

XX Homo sapiens.

XX WO2003025148-A2.

XX 27-MAR-2003.

XX 19-SEP-2002; 2002WO-US029964.

XX 19-SEP-2001; 2001US-0323739P.

XX 13-SEP-2002; 2002US-00323739.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Asundi V, Goodrich RW, Ren P, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;
PI Haley-Vicente D;

XX WPI; 2003-354603/33.
DR P-PSDB; AD121579.

XX New polynucleotides and secreted proteins, useful for treating myeloid or
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve
PT tissue growth or regeneration, in wound healing, and in tissue repair and
PT replacement.

XX Example 2; SEQ ID NO 610; 156pp; English.

XX The invention relates to an isolated polynucleotide encoding a

CC polypeptide with biological activity. The polynucleotides and

CC polypeptides are useful in diagnostics, forensics, gene mapping,

CC identification of mutations responsible for genetic disorders and other

CC traits, to assess biodiversity, as nutritional sources or supplements.

CC The polynucleotides may also be used as molecular weight markers,
CC chromosome markers or map related gene positions, or as an antigen to
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are
CC useful for raising antibodies, as markers for tissues in which the
CC corresponding polypeptide is expressed, for re-engineering damaged or
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in
CC bone cartilage, tendon, ligament and/or nerve tissue growth or
CC regeneration, in wound healing, in tissue repair and replacement, in
CC healing of burns, incisions and ulcers, and in treating cancer. The
CC present sequence represents a novel human expressed sequence tag, EST.
XX

SQ Sequence 861 BP; 216 A; 214 C; 265 G; 166 T; 0 U; 0 Other;

Query Match 54.1%; Score 827.8; DB 10; Length 861;
Best Local Similarity 98.5%; Pred. No. 3.9e-210;
Matches 846; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 30 CGGCTCTCGCTTCCGAGCGCGGACGCGCGCGCTGGGGGAGGAGGCGCAAGCGAGCGG 89
Db 2 CGACTCTTTCGTCGCGAGCGCGGACGCGCGCGCTGGGGGAGGAGGCGCAAGCGAGCGG 61
Qy 90 GCGATGGCTCCGCGGGCACTTCCCGGGTCCCGCTCTAGCCGCTGCTCTTCTGTGGGA 149
Db 62 GCGATGGCTCCGCGGGCACTTCCCGGGTCCCGCTCTAGCCGCTGCTCTTCTGTGGGA 121
Qy 150 GCGCGCTGAGTTCGCGCGCTGGTCCCGGCAATGGGAGGAGGCGCAATTCGACTCC 209
Db 122 GCGCGCTGAGTTCGCGCGCTGGTCCCGGCAATGGGAGGAGGCGCAATTCGACTCC 181
Qy 210 AGAACAGAGACGACCCCGTCGCGCAACGATCTGGGAATGGACACCCAGATATATT 269
Db 182 AGAACAGAGACGACCCCGTCGCGCAACGATCTGGGAATGGACACCCAGATATATT 241
Qy 270 GCATACGCGTGTGCTGCTGTTTATCATGGTCTCTTTGGCGTCTCATTTGCGCAC 329
Db 242 GCATACGCGTGTGCTGCTGTTTATCATGGTCTCTTTGGCGTCTCATTTGCGCAC 301
Qy 330 CTGCTTAAGAGAAAGGCTATCGTTGACACAGACAGACAGACAGATATCGAAGAGAA 389
Db 302 CTGCTTAAGAGAAAGGCTATCGTTGACACAGACAGACAGACAGATATCGAAGAGAA 361
Qy 390 AAGGTTGAAAAGATAGAAATGAAATGACAGTGTGAATGAAAACAGTGACACTGTTGGGCAA 449
Db 362 AAGTTGAAAAGATAGAAATGAAATGACAGTGTGAATGAAAACAGTGACACTGTTGGGCAA 421
Qy 450 ATCGTCCACTACATCATGAAAAATGAAGCGAATGCTGATGTCTTAAAGCGATGGTAGCA 509
Db 422 ATCGTCCACTACATCATGAAAAATGAAGCGAATGCTGATGTCTTAAAGCGATGGTAGCA 481
Qy 510 GATAACAGCCCTGTATGATCCTGAAAGCCCGTGACCCCGAGCACACCA- GGGAGCCGCC 568
Db 482 GATAACAGCCCTGTATGATCCTGAAAGCCCGTGACCCCGAGCACACCA- GGGAGCCGCC 541
Qy 569 AGTGAGTCTCTGGGCTTTGTTCACAGGGGGGAGCCAGGGAAGCACGCTGTGTGCCATCA 628
Db 542 AGTGAGTCTCTGGGCTTTGTTCACAGGGGGGAGCCAGGGAAGCACGCTGTGTGCCATCA 601
Qy 629 TCTGCATACCGTGGGCGGTGTTGTGAGAGGGATGTGTGTCGCGTGTAGGCAACAAGCG 688
Db 602 TCTGCATACCGTGGGCGGTGTTGTGAGAGGGATGTGTGTCGCGTGTAGGCAACAAGCG 661
Qy 689 GTGGCACTTTATAAAGCCCACTAACAGTCCAGAGAGAGACACCGCGCCCAAGGCGA 748
Db 662 GTGGCACTTTATAAAGCCCACTAACAGTCCAGAGAGAGACACCGCGCCCAAGGCGA 721
Qy 749 GGTCAAGCTCTCTCTGTGGCAGATTTAGAGTTACAAAAGTGGAGCACAAGTCAAAACCA 808
Db 722 GGTCAAGCTCTCTCTGTGGCAGATTTAGAGTTACAAAAGTGGAGCACAAGTCAAAACCA 781
Qy 809 GAAGGAACGGGAAGCCCTGATGTCTGTAGTGGGGCTGAACCCGTCATATGGGGAGGTGCC 868
Db 782 CAAGGAACGGGAAGCCCTGATGTCTGTATGGGGCTGAACCCGTCATATGGGGAGGTGCC 841

CC nucleic acid molecule; a nucleic acid composition comprising a carrier or
CC a buffer and one or more compositions comprising the nucleic acid
CC molecule, vector or host cell; a substantially purified polypeptide; an
CC animal injected with the polypeptide; a polypeptide composition
CC comprising the polypeptide molecule and a carrier or buffer; a cell
CC culture medium comprising the polypeptide or transfected cells
CC transfected with the polynucleotide; making a transformed, transfectant,
CC transduced, or infected host cell; synthesising Nanodiscs simultaneously
CC and for synthesising a series of simultaneously-synthesised Nanodiscs
CC sequentially utilising a dynamic system; preparing a hydrophobic protein
CC for determination of crystal structure; immunising a non-human animal;
CC screening for modulators of hydrophobic protein activity; a diagnostic
CC kit; determining the presence of the nucleic acid molecule or its
CC complement; determining the presence of an antibody to the polypeptide in
CC a sample; an antibody specifically recognising, binding to or modulating
CC the biological activity of at least one polypeptide encoded by a nucleic
CC acid molecule or its biologically active fragment; an antibody
CC composition comprising the antibody and a carrier; a bacteriophage, where
CC the antibody is displayed on the bacteriophage; a bacterial cell
CC comprising the bacteriophage; a non-human animal injected with the
CC antibody composition; a host cell that secretes the antibody; making an
CC antibody; diagnosing a disease, disorder, syndrome, or condition
CC comprising cancer, or proliferative, inflammatory, immune, metabolic,
CC bone, CNS, genetic, bacterial and viral diseases, disorders, syndromes or
CC conditions in a patient; a modulator composition comprising a modulator
CC and a carrier; gene therapy; prophylactic or therapeutic treatment of a
CC subject; an isolated modified cell comprising at least one first
CC heterologous nucleic acid molecule, where the first heterologous nucleic
CC acid molecule comprises a first polynucleotide sequence that encodes a
CC first polypeptide; a non-human animal deficient in the polypeptide or
CC that over-expresses the polypeptide; isolated tissues derived from the
CC non-human animal; and one or more cells derived from the non-human
CC animal. The nucleic acid is useful in preparing a composition for
CC diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
CC This sequence encodes a novel human polypeptide of the invention.

XX Sequence 348 BP; 34 A; 121 C; 146 G; 47 T; 0 U; 0 Other;

Query Match 13.4%; Score 172.6; DB 13; Length 348;
Best Local Similarity 97.8%; Pred. No. 1.8e-39;
Matches 175; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 CCACGCGTCCGCGCCGCGCTCCGAGCGGCTCTGCTTCCGAGCGCGGACGCGCG 61
DB 42 CCATCGATCAGCCGCGCGCTCCGAGCGGCTCTGCTTCCGAGCGCGGACGCGCG 101
QY 62 CCCTGGGGAGGAGGCGAGCGAGCGGCGATGGCTCCGCGGCACTCCCGGGTCCGC 121
DB 102 CCCTGGGGAGGAGGCGGAGCGAGCGGCGGATGGCTCCGCGGCACTCCCGGGTCCGC 161
QY 122 CGTCTAGCCGCTCTGCTTCTGCGGAGGCGCGTCTGAGTTCGCGGCTCGGCTCCGG 180
DB 162 CGTCTAGCCGCTCTGCTTCTGCGGAGGCGCGTCTGAGTTCGCGGCTCGGCTCCGG 220

RESULT 14
ABQ19006
ID ABQ19006 standard; DNA; 694 BP.
XX ABQ19006;
XX
XX
DT 12-JUL-2002 (first entry)
XX
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 5597.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.

OS Homo sapiens.

XX WO200218632-A2.

PN

XX 07-MAR-2002.
PD
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
XX 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX
DR
XX

PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.

XX Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention

XX Sequence 694 BP; 74 A; 86 C; 302 G; 232 T; 0 U; 0 Other;

Query Match 8.9%; Score 115.4; DB 6; Length 694;
Best Local Similarity 81.2%; Pred. No. 1.2e-22;
Matches 134; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 16 CGCGCGTCCGAGCGGCTCTGCCCTCCGAGCGCGGACGCGCGCTCGGGGAGGAG 75
DB 246 CGTCCGTTCCGAGCGGTTTGTGTTTTTCGAGCGCGGACGCGCGCTTTGGGGGAGGAG 305
QY 76 GCGGAGCGAGCGGCGGATGGCTCCGCGGCGACTCCCGGGGTCCGCGCTCTACCGCTG 135
DB 306 GCGGAGCGAGCGGCGGATGGTTTCGCGGGTATTTTCGGGGTTCGTCTTTAGTCGTTG 365
QY 136 CTGTCTTCGCGGAGCGCGCTGAGTTCGCGGCTGCTGGTGGCTCCCG 180
DB 366 TTGTTTTCGTTGGGAGGCGCTGCTGAGTTCGTGTTGTTGTTCCG 410

RESULT 15
ABQ19007/c
ID ABQ19007 standard; DNA; 694 BP.

XX ABQ19007;

XX

DT 12-JUL-2002 (first entry)

XX

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 5598.

XX

KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;

KW SNP; cell differentiation; ds.

XX Homo sapiens.

XX WO200218632-A2.

XX 07-MAR-2002.

XX 01-SEP-2001; 2001WO-EP010074.

XX 01-SEP-2000; 2000DE-01043826.

XX 05-SEP-2000; 2000DE-0104543.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Guetig D;

XX WPI; 2002-371829/40.

XX Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.

XX Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNPs); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention

XX SQ Sequence 694 BP; 232 A; 302 C; 86 G; 74 T; 0 U; 0 Other;

Query Match	8.9%	Score 115.4;	DB 6;	Length 694;
Best Local Similarity	81.2%	Pred. No. 1.2e-22;		
Matches 134;	Conservative 0;	Mismatches 31;	Indels 0;	Gaps 0;

QY	16	CGCGGGCTCCGAGCGGCTTGCCCTCCGAGCGCGGACCGCGCCCTGGGGGAGGAG	75
Db	449	CGTCGGTTTCGAGCGGTTTTGTTTTTCGAGCGCGGACCGCGCGTTTTGGGGGAGGAG	390
QY	76	GCGGAGCGGACGGCGATCGCTCCGCGGCGGACCTCCCGGGTCCCGCTCTAGCCGCTG	135
Db	389	GCGGAGCGGACGGCGGATCGTTTCGCGGGTATTTTCGGGGTTCTGCTTTTGTTCGTTG	330
QY	136	CTGCTTTCGGGGAGGCGCGTGTGAGTTCGCGGCTGGTGGCTCCGG	180
Db	329	TTGTTTCGTTGGGAGGCGCTGTGAGTTCGTTGGTGGTTTCGG	285

Search completed: February 23, 2006, 14:48:06
Job time : 791 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 14:48:23 ; Search time 4935 Seconds
(without alignments)
12239.539 Million cell updates/sec

Title: US-10-620-562-1

Perfect score: 1291

Sequence: 1 cccacgcgtccggccgcg.....cttacgcaaaaaaaaaa 1291

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	855.2	66.2	898	5	BX463460
2	785.2	59.3	882	2	BE792154
3	736.8	58.6	882	5	BX423892
4	726.8	56.3	1000	3	BM919548
5	594.4	46.0	620	5	BQ807844
6	594.4	46.0	874	5	BU150311
7	570	44.2	577	8	DR004573
8	554.2	42.9	815	8	DN948289
9	538.2	41.7	684	3	BP438847
10	488.6	37.8	906	3	BI691144
11	479.6	37.1	626	8	DN382824
12	460.2	35.6	795	3	BI689796
13	454.6	35.2	680	5	BY754410
14	454.2	35.2	757	3	BI658107
15	449.4	34.8	672	5	BY754598
16	447.8	34.7	813	6	CA459450
17	445.4	34.5	705	11	DQ043383
18	439.4	34.0	710	5	BY735770
19	407.4	31.6	612	2	BB619564
20	405.6	31.4	705	11	DQ043384
21	387.2	30.0	578	2	BE282422
22	385.6	29.9	660	2	BB612565

23	384.4	29.8	661	2	BB624998
24	383.8	29.7	624	7	CF899514
25	380	29.4	873	6	CA458776
26	368.4	28.5	642	2	BG975812
27	367.6	28.5	652	5	BY727150
28	364.2	28.2	1013	2	BG862046
c	359	27.8	441	1	AA782933
29	336.4	26.1	722	7	CF950164
30	319	24.7	464	7	CK334279
31	318.4	24.7	476	1	AI593167
32	315.2	24.4	466	5	BY256640
33	314.6	24.4	643	2	BI113590
34	312.4	24.2	494	2	BF016184
35	309.6	24.0	490	1	AI788006
36	308.2	23.9	580	5	BY265553
37	306	23.7	779	3	BP156823
38	305	23.6	428	4	AK182372
39	288.6	22.4	973	5	BU234449
40	284.2	22.0	475	2	BB857593
41	278.8	21.6	441	5	BY273890
42	271.4	21.0	389	4	AK202598
43	271.4	21.0	765	7	CO559467
44	271	21.0	464	6	CA564115
45	271	21.0	464	6	CA564115

ALIGNMENTS

RESULT 1

BX463460

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

BX463460 898 bp mRNA linear EST 06-MAY-2004
CSODN002YB14 5-PRIME, mRNA sequence.
BX463460
BX463460.2 GI:47070031
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 898)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31033530.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 2573.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?8=CSODN002DA07QPI&c=2573.r.

FEATURES

source

1. .898

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODN002YB14"

/tissue_type="ADULT BRAIN"

/dev_stage="adult"

/clone_lib="Homo sapiens ADULT BRAIN"

/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

ORIGIN

```
Query Match      66.2%; Score 855.2; DB 5; Length 898;
Best Local Similarity 97.1%; Pred. No. 8.8e-221;
Matches 873; Conservative 15; Mismatches 9; Indels 2; Gaps 2;

QY 14 CCGCCGGCTCCGAGCGGCTCTCCCTCCCGAGCGGGAGCGCGGCCCTCGGGGAGG 73
DB 1 CCGCCGGCTCCGAGCGGCTCTCCCTCCCGAGCGGGAGCGCGGCCCTCGGGGAGG 60

QY 74 AGGCGAAGCAGCAGCGG- CGATGCTCGGCGGCACTCCCGGGTCCCGCTCTAGCCG 132
DB 61 AGGCGAAGCAGCAGCGGCGATGCTCCCGGGCACTCCCGGGTCCCGCTCTAGCCG 120

QY 133 CTGCTGCTCTCGTGGAGGCGCGTGTAGTTCGCGCTGTGGCTCCGCAATGGGAGCA 192
DB 121 CTGCTGCTCTCGTGGAGGCGCGTGTAGTTCGCGCTGTGGCTCCGCAATGGGAGCA 180

QY 193 GCCGCACATTTGCACTCCAGAACAGAGACAGACCCCGTCCCGCAGCAAGATCTGGGAATG 252
DB 181 GCCGCACATTTGCACTCCAGAACAGAGACAGACCCCGTCCCGCAGCAAGATCTGGGAATG 240

QY 253 GACACCAGATATATTGCAATACCGCTTGTCCCTGTGTTCTTTATCATGGTCTCTTTG 312
DB 241 GACACCAGATATATTGCAATACCGCTTGTCCCTGTGTTCTTTATCATGGTCTCTTTG 300

QY 313 GCGTCTCTCATTTGCACTCTTAAGAAAGAGCTATCGTTGTACAAAGCAGCAGC 372
DB 301 GCGTCTCTCATTTGCACTCTTAAGAAAGAGCTATCGTTGTACAAAGCAGCAGC 360

QY 373 AAGATATCGAAGAGGAAAGGTTGAAAGATAGAAATGAATGACAGTGTGAATGAAACAA 432
DB 361 AAGATATCGAAGAGGAAAGGTTGAAAGATAGAAATGAATGACAGTGTGAATGAAACAA 420

QY 433 GTGACATGTTGGCAATGTGTCATCATATGAAATGAAATGAAATGAAATGAAATGAAATG 492
DB 421 GTGACATGTTGGCAATGTGTCATCATATGAAATGAAATGAAATGAAATGAAATGAAATG 480

QY 493 TAAAGGCGATGTTAGCAGATAACAGCTGTATGATCTGTAAGCCCGCTGACCCCGCAGCA 552
DB 481 TAAAGGCGATGTTAGCAGATAACAGCTGTATGATCTGTAAGCCCGCTGACCCCGCAGCA 540

QY 553 CACGAGGAGCGCCGCACTGAGTCTCGGCGCTTGTGTCACGAGGGGAGCGCAGGGAAGC 612
DB 541 CACGAGGAGCGCCGCACTGAGTCTCGGCGCTTGTGTCACGAGGGGAGCGCAGGGAAGC 600

QY 613 ACGTCTGTGGCATCATCTGCAATACGTTGGCGGTGTGTCAGAGGGATGTGTGTCATC 672
DB 601 ACGTCTGTGGCATCATCTGCAATACGTTGGCGGTGTGTCAGAGGGATGTGTGTCATC 660

QY 673 GGTGTAGGCACAGCGGTGGCACTTTATTAAGCCCACTTAACAGTCCAGAGAGCAGAC 732
DB 661 GGTGTAGGCACAGCGGTGGCACTTTATTAAGCCCACTTAACAGTCCAGAGAGCAGAC 720

QY 733 CACGGCCCAAGGCGAGTCACTGCTCTTCTGTTGGCAGATTTAGAGTTACAAAAGTGG 792
DB 721 CACGGCCCAAGGCGAGTCACTGCTCTTCTGTTGGCAGATTTAGAGTTACAAAAGTGG 780

QY 793 AGCACAAGTCAACAGAGAAAGAGAGAGAGCTGTATGTTAGTGGGCTGAAACCG 852
DB 781 AGCACAAGTCAACAGAGAAAGAGAGAGAGAGCTGTATGTTAGTGGGCTGAAACCG 840

QY 853 TCAATGGGAGGTGCGCGCAACCTCTGAAGAGAAACCGAGTGGCAGAGGTAGCAG 911
DB 841 TCAATGGGAGGTGCGCGCAACCTCTGAAGAGAAACCGAGTGGCAGAGGTAGCAG 898
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RESULT 2
LOCUS BE792154
DEFINITION BE792154 882 bp mRNA linear EST 20-SEP-2000
ACCESSION BE792154
VERSION BE792154.1 GI:10213352
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KEYWORDS

EST.
Homo sapiens (human)
Homo sapiens

ORGANISM
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 882)

NTN-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe-x@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: L1CM780 row: j column: 12

High quality sequence stop: 825.

FEATURES

Location/Qualifiers

1..882

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3936491"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 7"

/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAGGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 59.3%; Score 765.2; DB 2; Length 882;
Best Local Similarity 99.5%; Pred. No. 2.5e-196;
Matches 778; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 26 GGAGCGGCTCTGCTTCCCGAGCGCGGAGCGCGGCCCTGGGGAGAGGCGGAGCGGA 85

DB 1 GGAGCGGCTCTGCTTCCCGAGCGCGGAGCGCGGCCCTGGGGAGAGGCGGAGCGGA 60

QY 86 CGCGGCGATGGCTCCGCGGCGACTCCCGGGGTCCCGCGTCTAGCCGCTGCTGCTTCGT 145

DB 61 CGCGGCGATGGCTCCGCGGCGACTCCCGGGGTCCCGCGTCTAGCCGCTGCTGCTTCGT 120

QY 146 GGGAGGCGCGGTGAGTTTCGCGCTGCTGGTGGTCCGGACAATGGGAGAGCGCACATTGCA 205

DB 121 GGGAGGCGCGGTGAGTTTCGCGCTGCTGGTGGTCCGGACAATGGGAGAGCGCACATTGCA 180

QY 206 CTCAGAACAGAGACGACGCCCGTCCGCCAGCAGATACATGGGATCGACACCCAGATA 265

DB 181 CTCAGAACAGAGACGACGCCCGTCCGCCAGCAGATACATGGGATCGACACCCAGATA 240

QY 266 TATTGCATACGCGTTCCTGCTGTTTATCATGGGTCTCTTTGGGCTCTCTCATTTG 325

DB 241 TATTGCATACGCGTTCCTGCTGTTTATCATGGGTCTCTTTGGGCTCTCTCATTTG 300

QY 326 CCACCTGCTTTAAGAAAGAGGCTATCGTTGTACAAAGAGAGCAGAGCAAGATATCGAAGA 385

DB 301 CCACCTGCTTTAAGAAAGAGGCTATCGTTGTACAAAGAGAGCAGAGCAAGATATCGAAGA 360

QY 386 GGAAGAGTTGAAAGATAGATTAATGATGACGTGTGAATGAAACAGTGCACACTGTTGG 445

DB 361 GGAAGAGTTGAAAGATAGATTAATGATGACGTGTGAATGAAACAGTGCACACTGTTGG 420

QY 446 GCAAAATCGTCCACTACATCATGAAATGAAGCGATGCTGATGCTCTTAAAGCGGATGGT 505

Db 421 GCAATCGTCACATACATCATGAATAATGAAGCGAATGCTGATCTCTAAAGCGATGGT 480
Qy 506 AGCAGATAAACAGCGCTGATGATCTCTGAAGCCCGGTGACCCCGACAGCAGCAGCAGGAGCCC 565
Db 481 AGCAGATAAACAGCGCTGATGATCTCTGAAGCCCGGTGACCCCGACAGCAGCAGGAGCCC 540
Qy 566 GCCAGTGAGTCTCTGGGCTTTGTCCACGAGGGGAGCGCCAGGGAAGCAGCTGTGTGGCCA 625
Db 541 GCCAGTGAGTCTCTGGGCTTTGTCCACGAGGGGAGCGCCAGGGAAGCAGCTGTGTGGCCA 600
Qy 626 TCATCTGCATACGCTGGGCGGTGTTGTCGAGAGGGATGTGTCTCATCGGTGAGGCACAA 685
Db 601 TCATCTGCATACGCTGGGCGGTGTTGTCGAGAGGGATGTGTCTCATCGGTGAGGCACAA 660
Qy 686 GCGGTGGCACCTTTATAAAGCCCACTAAACAAGTCCAGAGAGAGCAGACACCGGCCCAAGG 745
Db 661 GCGGTGGCACCTTTATAAAGCCCACTAAACAAGTCCAGAGAGAGCAGACACCGGCCCAAGG 720
Qy 746 CGAGGTACGCTCTCTTTCTGTGTGGCAGATTTAGA-GTTTAAAGAGTGAGAGCAGATGCA 804
Db 721 CGAGGTACGCTCTCTTTCTGTGTGGCAGATTTAGAAGTTTACAAAAGTGAGAGCAGATGTA 780
Qy 805 AC 806
Db 781 CC 782

RESULT 3
LOCUS BX423892 882 bp mRNA linear EST 01-MAY-2004
DEFINITION BX423892 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CSODN002YB14 5-PRIME, mRNA sequence.
ACCESSION BX423892
VERSION BX423892.2 GI:46932572
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (bases 1 to 882)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30655585.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 2573.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS1AN001ZD08QPI&c=2573.r.
Location/Qualifiers
1..882
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN002YB14"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

FEATURES
source
1..882
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN002YB14"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match 58.6%; Score 756.8; DB 5; Length 882;
Best Local Similarity 96.7%; Pred. No. 4.8e-194;
Matches 803; Conservative 9; Mismatches 13; Indels 5; Gaps 4;
Qy 14 CCGCGCGGCTCCGAGCGGCTCTGCGTTCGCGAGCGGGGACGCGGCGCCCTGGGGAGG 73
Db 1 CCGCGCGGCTCCGAGCGGCTCTGCGTTCGCGAGCGGGGACG-GNCGCCCTGGGGAGG 59
Qy 74 AGGCGGAAGGACGCGCGG-CGATGGCTCCGCGGGGCACTCCCGGGGTCCGCGCTCTAGCCG 132
Db 60 AGGCGGAAGGACGCGCGGCGATGGCTCCGCGGGGCACTCCCGGGGTCCGCGCTCTAGCCG 119
Qy 133 CTGCTGTCTTCGTGGGAGGCGCGGTGAGTTCCGCGGTGGTGGTCCGAGCAATGGGAGCA 192
Db 120 CTGCTGTCTTCGTGGGAGGCGCGGTGAGTTCCGCGGTGGTGGTCCGAGCAATGGGAGCA 179
Qy 193 GCGGCACATTTGCATCTCCAGAACAGAGACGACCCCGTCCGCGAGCAATGCTGGGAATG 252
Db 180 GCGGCACATTTGCATCTCCAGAACAGAGACGACCCCGTCCGCGAGCAATGCTGGGAATG 239
Qy 253 GACACCCAGAAATATATTCGATACCGCTTGTCCCTGTGTTCTTTATCATGGGTCTCTTTG 312
Db 240 GACACCCAGAAATATATTCGATACCGCTTGTCCCTGTGTTCTTTATCATGGGTCTCTTTG 299
Qy 313 GCGTCTCATTTGCGCACCTGCTTAAGAGAAAGGCTATCGTTGTATCAACAGAGCAGAGC 372
Db 300 GCGTCTCATTTGCGCACCTGCTTAAGAGAAAGGCTATCGTTGTATCAACAGAGCAGAGC 359
Qy 373 AAGTATTCGAGAGGAAAGGTTGAAAGATAGAAATGAAATGACAGTGTGAATGAAACA 432
Db 360 AAGTATTCGAGAGGAAAGGTTGAAAGATAGAAATGAAATGACAGTGTGAATGAAACA 419
Qy 433 GTGACACTGTTGGGCAAAATCGTCCACTACATCATGAAAAATGAAGCGAATGCTGATGCT 492
Db 420 GTGACACTGTTGGGCAAAATCGTCCACTACATCATGAAAAATGAAGCGAATGCTGATGCT 479
Qy 493 TAAAGGCGATGGTAGCAGATAACAGCTGTATGATCTCTGAAAGCCCGTACCCCGAGCA 552
Db 480 TAAAGGCGATGGTAGCAGATAACAGCTGTATGATCTCTGAAAGCCCGTACCCCGAGCA 539
Qy 553 CACCAGGAGCGCCCGCAGTGAGTCTCGGCGCTTTGTCCAGCGGGGAGCGCCAGGAGC 612
Db 540 CACCAGGAGCGCCCGCAGTGAGTCTCGGCGCTTTGTCCAGCGGGGAGCGCCAGGAGC 599
Qy 613 ACGTCTGTGGCCATCATCTGATACGCTGGGCGGTGTTGTCGAGAGGATGTTGTGTCATC 672
Db 600 ACGTCTGTGGCCATCATCTGATACGCTGGGCGGTGTTGTCGAGAGGATGTTGTGTCATC 659
Qy 673 GGTGTAGGCACAACGCGGTGGCACTTTTATAAAGCCCACTTAAAGTCCAGAGAGCAGAC 732
Db 660 GGTGTAGGCACAACGCGGTGGCACTTTTATAAAGCCCACTTAAAGTCCAGAGAGCAGAC 719
Qy 733 CACGCGCCCAAGCGAGGTCAAGTCTCTTTCTGTCGAGATTTAGAGTTACAAAAGTGG 792
Db 720 CACGCGCCCAAGCGAGGTCAAGTCTCTTTCTGTCGAGATTTAGAGTTAC-AAARKKG 778
Qy 793 AGCAAGAGTCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 842
Db 779 AGCAAGAGTCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 826

RESULT 4
LOCUS BM919548
DEFINITION BM919548 1000 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6761913 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748847
5', mRNA sequence.
ACCESSION BM919548
VERSION BM919548.1 GI:19369927
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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Db 1 GGAGCGGCTCTGCTTCCCGAGCGCGCCCTGGGGAGGAGGGCGA 60
Qy 86 CGGGCGATGGCTCCCGGGGCACTCCCGGGGTCCTAGCCGCTGTCTTCGT 145
Db 61 CGGGCGATGGCTCTCGGGGCACTCCCGGGGTCCTAGCCGCTGTCTTCGT 120
Qy 146 GGAGGGCGCGTGGATTCGCGGTCGTGGTTCGGGCAATGGGAGCAGCGCAATGCA 205
Db 121 GGGAGGGCGCGTGGATTCGCGGTCGTGGTTCGGGCAATGGGAGCAGCGCAATGCA 180
Qy 206 CTCAGAACAGAGACGACCGCGCCGACGACGATCTGGGATGACACCCAGATA 265
Db 181 CTCAGAACAGAGACGACCGCGCCGACGACGATCTGGGATGACACCCAGATA 240
Qy 266 TATTGCATAGCGCTTGTCTTCTTATCATGGGTCTCTTTGGCGTCTCATTTG 325
Db 241 TATTGCATAGCGCTTGTCTTCTTATCATGGGTCTCTTGGCGTCTCATTTG 300
Qy 326 CCACCTGCTTAAAGAAAGGCTATCTGTGTACAAAGAGCAGAGCAAGATATCGAAGA 385
Db 301 CCACCTGCTTAAAGAAAGGCTATCTGTGTACAAAGAGCAGAGCAAGATATCGAAGA 360
Qy 386 GGAAGAGTTGAAAGATAGATTTGAATGACAGTGTGAATGAAACAGTGCACATGTTG 445
Db 361 AGAAAGGTTGAAAGATAGATTTGAATGACAGTGTGAATGAAACAGTGCACATGTTG 420
Qy 446 GCAATCGTCCACTACATCATGAAATGAAGCAATGCTGTCTTAAAGGCGATGGT 505
Db 421 GCAATCGTCCACTACATCATGAAATGAAGCAATGCTGTCTTAAAGGCGATGGT 480
Qy 506 AGCAGATAACAGCGCTGTATGATCTGAAAGCCCGTGCACCCAGCAGCAGGAGGCC 565
Db 481 AGCGGATAACAGCGCTGTATGATCTGAAAGCCCGTGCACCCAGCAGCAGGAGGCC 540
Qy 566 GCAGTGAGTCTGGGCTTGTACAGGGGGAGCCAGGAGCAGTCTGTGGCCA 625
Db 541 ACCGCTGAGTCTGGGCTTGTACAGGGGGAGCCCGGAGGAGCAGTCTGTGGCCA 600
Qy 626 TCATCTGCATACGTTGGGCG 645
Db 601 TCATCTGCATACGTTGGGCG 620
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RESULT 6
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LOCUS BUI50311 874 bp mRNA linear EST 03-SEP-2002
DEFINITION AGENCOURT_8121018 Lupski_dorsal_root_ganglion Homo sapiens cDNA
clone IMAGE:6178627 5', mRNA sequence.
ACCESSION BUI50311
VERSION BUI50311.1 GI:22663843
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 874)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM3558 row: h column: 20
High quality sequence stop: 592.
Location/Qualifiers
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FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6178627"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski_dorsal_root_ganglion"
/notes="Vector: pCMV-Sport6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCG-3' and
5'-GACTAGTTCTAGATCGGAGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
ORIGIN
Query Match 46.0%; Score 594.4; DB 5; Length 874;
Best Local Similarity 98.9%; Pred. No. 6.4e-150;
Matches 609; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
Qy 179 GGCAATGGGAGCAGCGCACATTGCATCCAGAAACAGAGACGACCCCGTCCGCGCA 238
Db 182 GTACATGGGAGCAGCGCACATTGCATCCAGAAACAGAGACGACCCCGTCCGCGCA 241
Qy 239 CGATATCTGGAAATGGACACCCAGATATATTCATACGCGCTGTCTCTGTCTTTAT 298
Db 242 CGATATCTGGAAATGGACACCCAGATATATTCATACGCGCTGTCTCTGTCTTTAT 301
Qy 299 CATGGGCTCTTTGGGCTCTCTTTGGGCTCTCTTTGGGCTCTCTTTGGGCTCTCTTAC 358
Db 302 CATGGGCTCTCTTTGGGCTCTCTTTGGGCTCTCTTTGGGCTCTCTTTGGGCTCT 361
Qy 359 AACAGAGCAGAGCAAGATATCGAAGAGGAAAGGTTGAAAGATAGATATGAATGACAG 418
Db 362 AACAGAGCAGATAGCAAGATATCGAAGAGGAAAGGTTGAAAGATAGATATGAATGACAG 421
Qy 419 TGTGAATGAAACAGTGACACTGTGTGGGCAAAATCGTCCATCATCATGAAAAATGAAGC 478
Db 422 TGTGAATGAAACAGTGACACTGTGTGGGCAAAATCGTCCATCATCATGAAAAATGAAGC 481
Qy 479 GAATGCTGATGTCTTAAAGCGGATGTAGCAGATAACAGCTGTATGATCTCTGAAGGCC 538
Db 482 GAATGCTGATGTCTTAAAGCGGATGTAGCAGATAACAGCTGTATGATCTCTGAAGGCC 541
Qy 539 CGTGACCCCGCAGCACACCGAGGAGCCGCGAGTGAGTCTCTGGGCTTTTGTCCAGGGGG 598
Db 542 CGTGACCCCGCAGCACACCGAGGAGCCGCGAGTGAGTCTCTGGGCTTTTGTCCAGGGGG 601
Qy 599 GAGCGCCAGGAGCAGCTGTGTGGCCATCATCTGTCATACCGTGGCGGCTGTGTGCGAGAG 658
Db 602 GAGCGCCAGGAGCAGCTGTGTGGCCATCATCTGTCATACCGTGGCGGCTGTGTGCGAGAG 661
Qy 659 GGATGTGTCTCATCGGTGTAGGACCAAGCGGTGGCACTTTTAAAGCCCACTAACAGTC 718
Db 662 GGATGTGTCTCATCGGTGTAGGACCAAGCGGTGGCACTTTTAAAGCCCACTAACAGTC 721
Qy 719 CAGAGAGCAGACACCGCGCCGAGGAGTCA-CGGTCTCTTCTGTGGCAGATTTA 777
Db 722 CAGAGAGCAGACACCGCGCCGAGGAGTCA-CGGTCTCTTCTGTGGCAGATTTA 781
Qy 778 GAGTTACAAAAGTGA 793
Db 782 GAGTTACAAAAGTGA 797
RESULT 7
DR004573
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LOCUS
 DEFINITION DR004573 577 bp mRNA linear EST 17-MAY-2005
 TC104761 Human placenta, large insert, pCMV expression library Homo
 sapiens cDNA clone TC104761 5' similar to Homo sapiens hypothetical
 protein LOC253981 (LOC253981), mRNA sequence.

ACCESSION
 VERSION DR004573.1 GI:66264446
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Birkett C., Cho J., Gau Y., Hamer R., Kelly S., Kovacs K., Liu L.,
 Liu X., Porter J., Sachs A., Shu Y., Sun Z., Wong J., Wu M.,
 Zhang X., Jay G. and He W.
 1 (bases 1 to 577)
 TITLE High-throughput cloning of full-length human cDNAs directly from
 cDNA libraries optimized for large and rare transcripts
 JOURNAL Unpublished (2005)
 COMMENT Contact: Kovacs, KF
 High Throughput cDNA Cloning
 Origene Technologies, Inc. (www.origene.com)
 6 Taft Court, Suite 100, Rockville, MD 20850, USA
 Tel: 301 340 3188
 Fax: 301 340 8606
 Email: cDNA@origene.com
 This EST submission is part of an on-going human full-length
 cloning project at Origene Technologies, Inc.
 Please contact Origene for access.
 Origene Technologies, Inc.
 6 Taft Ct. Suite 100
 Rockville, MD 20850
 Tel: (301) 340-3188
 http://www.origene.com
 Seq primer: pCMV6 Spriime forward vector primer, Origene
 Technologies Inc.

FEATURES
 source
 1..577
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 /db_xref="taxon:9606"
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 /tissue_type="Placenta"
 /clone_lib="Human placenta, large insert, pCMV expression
 library"
 /note="Vector: pCMV6-XL4; Site 1: EcoR1; Site 2: Xho1/Sall
 compatible end ligatio; Oligo-dT primed reverse
 transcription optimized for large and GC rich mRNA
 transcripts, cDNA size selection, optimized ligation for
 large inserts into mammalian expression vector, random
 clones selected for end sequence verification of
 full-length genes"

ORIGIN
 Query Match 44.2%; Score 570; DB 8; Length 577;
 Best Local Similarity 99.7%; Pred. No. 2 5e-143;
 Matches 570; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 51 GGACACGGCGCCCTGGGGAGAGGGCGAAGCGACGCGCGATGGTCCGCGGCACCTC 110
 DB |||||
 6 GGGCGCGCGCCCTGGGGAGAGGGCGAAGCGACGCGCGATGGTCCGCGGCACCTC 65
 QY 111 CCGGGGTCCGCGCTCTAGCGCTGCTGTTCTGTTGGAGGCGCGCGTGGTTCGCGCTG 170
 DB |||||
 66 CCGGGGTCCGCGCTCTAGCGCTGCTGTTCTGTTGGAGGCGCGCGTGGTTCGCGCTG 125
 QY 171 GTGGCTCCCGACAATGGGAGCAGCCGCACATTGCATCCAGAACAGAGACGCCCGCTCG 230
 DB |||||
 126 GTGGCTCCCGACAATGGGAGCAGCCGCACATTGCATCCAGAACAGAGACGCCCGCTCG 185
 QY 231 CCAGCAACGATACTGGGAATGGACACCCAGAAATATATTCATACGCGCTGTCCCTGTG 290
 DB |||||
 186 CCCAGCAACGATACTGGGAATGGACACCCAGAAATATATTCATACGCGCTGTCCCTGTG 245

QY 291 TTCTTTATCATGGGTCTCTTTGGGCTCCTCATTTGCCACCTGCTTAAAGAAAGGCTAT 350
 DB 246 TTCTTTATCATGGGTCTCTTTGGGCTCCTCATTTGCCACCTGCTTAAAGAAAGGCTAT 305
 QY 351 CGTTGTACACAGACAGACAGCAGCAGATATCGAAGAGGAAAGGTTGAAAAGATAGAATTG 410
 DB 306 CGTTGTACACAGACAGACAGCAGCAGATATCGAAGAGGAAAGGTTGAAAAGATAGAATTG 365
 QY 411 AATGACAGTGTGAATGAAACACAGCAGCAGCTGTTGGGCAAAATCGTCCACTACATCATGAAA 470
 DB 366 AATGACAGTGTGAATGAAACACAGCAGCAGCTGTTGGGCAAAATCGTCCACTACATCATGAAA 425
 QY 471 AATGACAGCAGTCTGATGCTTTAAAGGCGATGGTAGCAGATACACAGCCTGTATGATCCT 530
 DB 426 AATGACAGCAGTCTGATGCTTTAAAGGCGATGGTAGCAGATACACAGCCTGTATGATCCT 485
 QY 531 GAAAGCCCCCTGAGCCCCCAGCACACACAGGAGCGCCGACGTGAGTCTCGGCGCTTTGTCA 590
 DB 486 GANAGCCCCCTGAGCCCCCAGCACACACAGGAGCGCCGACGTGAGTCTCGGCGCTTTGTCA 545
 QY 591 CAGGGGGGAGCGCCAGGAGAGCAGCTGTGTGG 622
 DB 546 CCAGGGGGGAGCGCCAGGAGAGCAGCTGTGTGG 577

RESULT 8
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 LOCUS
 DEFINITION AGENCOURT 50711126 NCI CGAP Pr49 Rattus norvegicus cDNA clone
 IMAGE:7932431 5', mRNA sequence.

ACCESSION
 VERSION DN948289
 KEYWORDS DN948289.1 GI:62971409
 SOURCE EST.
 ORGANISM Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Rattus.

REFERENCE
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Jeff Green/Patru Kondaiah, NCI.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LAM16355 row: k column: 21
 High quality sequence stop: 792.
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 /db_xref="taxon:10116"
 /clone="IMAGE:7932431"
 /sex="male"
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 /dev_stage="adult, 11 week"
 /lab_host="DH10B (T1 phage-resistant)"
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 /note="Organ: prostate; Vector: pCMV-SPORT6.1; Site 1:
 NotI; Site 2: EcoRV; Cloned unidirectionally. Primer:
 Oligo dT. Pool of 3 primary libraries: NCI CGAP_Pr30
 (ventral prostate from 11 wk male, 3 days


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Db 365 AAAGATAGAGATGAACGACAGCGTGAATGAAATAGTACACCGCTTGACAGAGTTGTCCA 424
Qy 458 CTACATCATGAAATGAAGGATGCTGATGCTTTAAAGCGGATGTAGCAGATAACAG 517
Db 425 CTACATCATGAAATGAAGCAATGCGGATGTTTGAAGGCAATGTGTGGCAGATAACAG 484
Qy 518 CCTGTATGATCCTGAAAGCCCGTGACCCCGACACACACAGGAGCCCGCAGTGAGTCC 577
Db 485 CTTGTATGATCCTGAAAGCCCTGTGACCCCGACACACTCTGGGAGCCCGCCGTTGGGCC 544
Qy 578 TGGGCCCTTGTACACAGGGGGAGCCGACAGGGAACAGCTCTGTGGCCATCATCTGCAATAC 637
Db 545 CGGSCCTTGTGACCGGGAGGACCCCGAGGAAACACATCTGTGGGCCACCATCTGCAAC 604
Qy 638 GTTGGGCGGTGTTGTGACAGAGGATGTGTGTCATCGGTGTAGGACAAAGCGTGGCACTT 697
Db 605 GGTGGGCGGTGCTGTCAAGCGGACGTTGTGTATCATGATGTANGCATAAGCGGTGGCACTT 664
Qy 698 TATAAGCCCACTAACAGT 717
Db 665 CATCAGACCTGCCAACAGT 684
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RESULT 10
BI691144 906 bp mRNA linear EST 18-SEP-2001
LOCUS 60314531F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5354671 5',
DEFINITION mRNA sequence.
ACCESSION BI691144
VERSION BI691144.1 GI:15653773
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 906)
NTH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
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Query Match 37.8%; Score 488.6; DB 3; Length 906;
Best Local Similarity 82.4%; Pred. No. 3.6e-121;
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Qy 216 GAGACGACCC- - -CGTCGCCCGCAGCAAGATCTAGTGGGAATGGACACCCAGAGATATATTGCA 272
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Qy 573 AGTCTGGGCTTTTGTCCACGAGGGGGAGCGCCAGGGAAGCACGCTCTGTGGCCATCATCTG 632
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Qy 633 CATACGCTGGGCGGTGTTGTCGAGAGGATGTGTGTCATCGGTGTAGGACAAAGCGGTGG 692
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DEFINITION DN382824 626 bp mRNA linear EST 07-MAR-2005
LIB38534_030_A09_T7_1 LIB38534 Canis familiaris cDNA clone
LIB38534_30_A09_mRNA sequence.
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VERSION DN382824.1 GI:60564044
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
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REFERENCE 1 (bases 1 to 626)
AUTHORS Staten,N.R.
TITLE Direct Submission (Staten,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
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Best Local Similarity 86.2%; Pred. No. 9.3e-119;
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Qy 183 AATGGGAGAGCCGCCACATGCACTCCAGAACAGACGACCCCGTCCGCCAGCAACGAT 242
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Qy 423 AATGAAACAGTGCACCTGTTGGCAATCGTCCATCATCATGATGAAATAATGAAGCGAAT 482
Db 372 AATGAAATAGTGCACCGTTGGCGAGATTGTCAGTACATCATGATGAAATAATGAAGCAAC 431
Qy 483 GCTGATCTTAAAGGCGATGGTAGCAGATACAGCCTGATGATCTCTGAAAGCCCGTG 542
Db 432 GTTGATGTTTAAAGGCAATGGTAGCAGATACAGCCTGGGGGACCCCTGAAAGCCCTGTG 491
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Db 492 ACTCCAGCACTCTGGAGCCCGCCCTGTGAGCCCGGGGCCCTTGTCCCAAGGAGGACC 551
Qy 603 CCAGGGAAGCAGCTCTGTGGCCATCATCTGCATACGGTGGGCGGTGTTGTGAGAGGGAT 662
Db 552 CCAGGAAACACATCTATGGCCACCATCTACACACAGTANGAGGTGCTGTTGAGAGGGAC 611
Qy 663 GTGTGTCATCGTGT 677
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RESULT 12
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DEFINITION mRNA sequence.
ACCESSION BI689796
VERSION BI689796.1 GI:15652425
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 795)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1905 row: c column: 03
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ORIGIN

Query Match 35.6%; Score 460.2; DB 3; Length 795;
Best Local Similarity 79.4%; Pred. No. 1.8e-113;
Matches 620; Conservative 0; Mismatches 153; Indels 8; Gaps 6;

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Qy 211 GAACAGAGAGACCCC---CGTCCGCCAGCAACGATCTGGGAATGACACCCAGAAATA 267
Db 137 GAGCAGAGACCACTCCATCGTCAACCACCAACACCTGGGAATGACACCCCGGAATACA 196
Qy 268 TTGCATAGCGCTTGTCCCTGCTGTTCTTTATCATGGGTCTCTTTGGCGTCTCTATTGCC 327
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Qy 328 ACCTGCTTAAAGAGAAAGGCTATCGTTGTACACAGAAAGCAGACAGATATCGAAGAGG 387
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Qy 448 AATCTGTCCTACATCATGAAATAATGAAGCGAATGCTGATGTTTAAAGCGATGTAG 507
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Qy      611  GCAGCTCTGGCGCATCATCTGCATACAGTGGGCGGTGTGTGCGAGAGGATGTGTCTCA 670
Db      612  GCATGCTGTGGTCATCATCTGCACACAGTGGGAGGTGTGCTGACGGGATGTGTGCCA 671
Qy      671  TCGGTGTAG 679
Db      672  GCGATGCGAG 680

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LOCUS   603285885F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5330037 5',
DEFINITION mRNA sequence.
ACCESSION BI658107
VERSION   BI658107.1 GI:15572343
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NTH-MGC http://mgi.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
        Email: cgabs-r@mail.nih.gov
        Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
        Ph.D.
        cDNA Library Preparation: Life Technologies, Inc.
        DNA Sequencing by: The I.M.A.G.E. Consortium (LMNL)
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        http://image.llnl.gov
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        providing samples: Lothar Hennighausen/Priscilla Furth.
        NIH Reference for transgenic model: Li et al., Cell Growth
        and Differentiation 7, 3-11 (1996)."
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ORIGIN

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ACCESSION BY754598
VERSION   BY754598.1 GI:27186642
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 672)
Okazaki.Y., Furuno.M., Kasukawa.T., Adachi.J., Bono.H., Kondo.S.,
Nikaido.I., Osato.N., Saito.R., Tomaru.Y., Hasegawa.Y., Nogami.A.,
Kiyosawa.H., Yagi.K., K., Tomaru.Y., Hasegawa.Y., Nogami.A.,
Hume.D.A., Quackenbush.J., Baldarelli.R., Hill.D.P., Bult.C.,
Batalov.S., Beisel.K.W., Blake.J.A., Bradt.D., Brusic.V.,
Chothia.C., Corbani.L.E., Cousins.S., Dalla.E., Dragani.T.A.,
Fletcher.C.F., Forrest.A., Frazer.K.S., Gaasterland.T.,
Gariboldi.M., Glissi.C., Godzik.A., Gough.J., Grimmond.S.,
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Kawaji.H., Kawasawa.Y., Kedzierzki.R.M., King.B.L., Konagaya.A.,
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Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sample, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, B. and Hayashizaki, Y.

TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL
Nature 420, 563-573 (2002)

PUBMED
12466851

COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resseq@riken.jp, URL: <http://genome.gsc.riken.jp/>
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Takashi Ishikawa (Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan) whose assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

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ORIGIN

Query Match 34.8%; Score 449.4; DB 5; Length 672;
Best Local Similarity 81.1%; Pred. No. 1.5e-110;
Matches 535; Conservative 0; Mismatches 122; Indels 3; Gaps 1;

QY 14 CCGCGCGCTCCGAGCGGCTCTGCCTTCCCGAGCGGACGCGGCGCCTCTGGGCGAGG 73
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QY 74 AGGGCGAAGCGACGCGCGCGATGCTCCGGGGCACTCCCGGGGTCCGCCGTCTCTAGCCGC 133
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1  EARLIER FILING DATE: 1997-06-06
2  EARLIER APPLICATION NUMBER: 60/048,915
3  EARLIER FILING DATE: 1997-06-06
4  EARLIER APPLICATION NUMBER: 60/049,019
5  EARLIER FILING DATE: 1997-06-06
6  EARLIER APPLICATION NUMBER: 60/048,970
7  EARLIER FILING DATE: 1997-06-06
8  EARLIER APPLICATION NUMBER: 60/048,972
9  EARLIER FILING DATE: 1997-06-06
10 EARLIER APPLICATION NUMBER: 60/048,916
11 EARLIER FILING DATE: 1997-06-06
12 EARLIER APPLICATION NUMBER: 60/049,373
13 EARLIER FILING DATE: 1997-06-06
14 EARLIER APPLICATION NUMBER: 60/048,875
15 EARLIER FILING DATE: 1997-06-06
16 EARLIER APPLICATION NUMBER: 60/049,374
17 EARLIER FILING DATE: 1997-06-06
18 EARLIER APPLICATION NUMBER: 60/048,917
19 EARLIER FILING DATE: 1997-06-06
20 EARLIER APPLICATION NUMBER: 60/048,949
21 EARLIER FILING DATE: 1997-06-06
22 EARLIER APPLICATION NUMBER: 60/048,974
23 EARLIER FILING DATE: 1997-06-06
24 EARLIER APPLICATION NUMBER: 60/048,883
25 EARLIER FILING DATE: 1997-06-06
26 EARLIER APPLICATION NUMBER: 60/048,897
27 EARLIER FILING DATE: 1997-06-06
28 EARLIER APPLICATION NUMBER: 60/048,898
29 EARLIER FILING DATE: 1997-06-06
30 EARLIER APPLICATION NUMBER: 60/048,962
31 EARLIER FILING DATE: 1997-06-06
32 EARLIER APPLICATION NUMBER: 60/048,963
33 EARLIER FILING DATE: 1997-06-06
34 EARLIER APPLICATION NUMBER: 60/048,877
35 EARLIER FILING DATE: 1997-06-06
36 EARLIER APPLICATION NUMBER: 60/048,878
37 EARLIER FILING DATE: 1997-06-06
38 EARLIER APPLICATION NUMBER: 60/070,923
39 EARLIER FILING DATE: 1997-12-18
40 EARLIER APPLICATION NUMBER: 60/092,921
41 EARLIER FILING DATE: 1998-07-15
42 EARLIER APPLICATION NUMBER: 60/094,657
43 EARLIER FILING DATE: 1998-07-30
44 NUMBER OF SEQ ID NOS: 1227
45 SOFTWARE: PatentIn Ver. 2.0
46 SEQ ID NO 56
47 LENGTH: 1603
48 TYPE: DNA
49 ORGANISM: Homo sapiens
50 FEATURE:
51 NAME/KEY: SITE
52 LOCATION: (328)
53 OTHER INFORMATION: n equals a,t,g, or c
54 FEATURE:
55 NAME/KEY: SITE
56 LOCATION: (336)
57 OTHER INFORMATION: n equals a,t,g, or c
58 FEATURE:
59 NAME/KEY: SITE
60 LOCATION: (341)
61 OTHER INFORMATION: n equals a,t,g, or c
62 FEATURE:
63 NAME/KEY: SITE
64 LOCATION: (788)
65 OTHER INFORMATION: n equals a,t,g, or c
66 US-09-205-258-56

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ay

QY 1137 GTGATATGAGGATAGAGGATTACTTGTGAGGCAATCTGGCATGTGGGATTTGGCAA 1196
DB 1142 GTGATATGAGGATAGAGGATTACTTGTGAGGCAATCTGGCATGTGGGATTTGGCAA 1201
QY 1197 ACTAGATTCACATCACCCACCATATATAGGCTTGCATTACACGAGGCGAGAGCACCTA 1256
DB 1202 ACTAGATTCACATCACCCACCATATATAGGCTTGCATTACACGAGGCGAGAGCACCTA 1261
QY 1257 GTGTGCTGCATCTTCTTACGCAAAAAA 1291
DB 1262 GTGTGCTGCATCTTCTTACGCAAAAAA 1296

RESULT 2

US-10-004-860-56
; Sequence 56, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 1603
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (336)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (341)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (788)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-004-860-56

Query Match 92.7%; Score 1196.6; DB 3; Length 1603;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1268; Conservative 5; Mismatches 13; Indels 9; Gaps 6;
QY 1 CCACCGGCTCGGCGCCCGGCTCCGAGGCGCTCTGCTCCGAGCGGCGGACGCGG 60
DB 7 CCACCGGCTCGGCGCCCGGCTCCGAGGCGCTCTGCTCCGAGCGGCGGACGCGG 64
QY 61 GCCTCGGGGAGGAGGCGGAGCGACCGCGGATGGCTCCGCGGCGACTCCCGGGTCCG 120
DB 65 GCCTCGGGGAGGAGGCGGAGCGACCGCGGATGGCTCCGCGGCGACTCCCGGGTCCG 123
QY 121 CCGTCTTAGCGCTGCTCTTCTGTGGGAGCGCGCGGATGGCTCCGCGGCGACTCCCGGGTCCG 180
DB 124 CCGTCTTAGCGCTGCTCTTCTGTGGGAGCGCGCGGATGGCTCCGCGGCGACTCCCGGGTCCG 183
QY 181 ACAATGGAGGAGCGCGGACATTTGCACTCCAGAACAGAGACGACCCCGTCCGCGGAGCAACG 240
DB 184 ACAATGGAGGAGCGCGGACATTTGCACTCCAGAACAGAGACGACCCCGTCCGCGGAGCAACG 243
QY 241 ATACTGGGATGGACCCGCAATATATTCATACGCGCTTGTCCCTGTCTTTATCA 300
DB 244 ATACTGGGATGGACCCGCAATATATTCATACGCGCTTGTCCCTGTCTTTATCA 303

QY 301 TGGGTCTCTTTGGGCTCTCAATTTGCCACCTGC---TTAAGAAAGAAAGGCTATCGTTGTA 357
DB 304 TGGGTCTCTTTGGGCTCTCAATTTNGCCAMCTNGCTTNAAGAAAGAAAGGCTATCGTTGTA 363
QY 358 CAACAGAGCAGAGCAGAGATATCGAAGAGG-AAAAGGTTGAAAGATAGAAATCAATGAC 416
DB 364 CAACAGAGCAGAGCAGAGATATCGAAGAGAAAGGTTGAAAGWTAGRAATTAATGAC 423
QY 417 AGTGTGAATGAAACACAGTGCACCTGTTTGGGCAATCGTCCACTACATCATCATGAAATGAA 476
DB 424 AGTGTGAATGAAACACAGTGCACCTGTTTGGGCAATCGTCCACTACATCATGAAATGAA 483
QY 477 GCGAATGCTGATGCTTTAAAGGCGATGTTAGCAGATAACAGCCTGTATGATCTCTGAAAGC 536
DB 484 GCGAATGCTGATGCTTTAAAGGCGATGTTAGCAGATAACAGCCTGTATGATCTCTGAAAGC 543
QY 537 CCGTGCACCCCGAGCAGCAGGAGGCGCCGAGTGTGAGTCTCTGGGCTTTGTACACGAGG 596
DB 544 CCGTGCACCCCGAGCAGCAGGAGGCGCCGAGTGTGAGTCTCTGGG-CTTTGTACACGAGG 602
QY 597 GGGACGCGCAGGAGGAGCAGCTCTGTGGCCATCATCTGCATACGGTGGGCGGTGTTGTGAG 656
DB 603 GGGACGCGCAGGAGGAGCAGCTCTGTGGCCATCATCTGCATACGGTGGGCGGTGTTGTGAG 662
QY 657 AGGATGTGTGTCATCGTGTAGGCAACAGCGGTGCGACATTTATAAAGCCCACTAAACAG 716
DB 663 AGGATGTGTGTCATCGTGTAGGCAACAGCGGTGCGACATTTATAAAGCCCACTAAACAG 722
QY 717 TCCAGAGAGAGCAGACCCGCGCCAGGCGAGTGTGAGTCTCTTCTGTGGCAGATTT 776
DB 723 TCCAGAGAGAGCAGACCCGCGCCAGGCGAGTGTGAGTCTCTTCTGTGGCAGATTT 782
QY 777 AGAGTTACAAAAGTGGAGCACAAGTCAAACAGAGGAAAGGAGAGCGCTGATCTCTGTT 836
DB 783 AGAGTTACAAAAGTGGAGCACAAGTCAAACAGAGGAAAGGAGAGCGCTGATCTCTGTT 842
QY 837 AGTGGGCTGAAACCGTCAATGGGAGGTCCGCGCAACACCTGTGAAAGAGAGAGCGAGT 896
DB 843 AGTGGGCTGAAACCGTCAATGGGAGGTCCGCGCAACACCTGTGAAAGAGAGAGCGAGT 902
QY 897 GGCACAGAGTAGCAGGTGAGCGCTGTTTGGTGACATTTGGGCGCAGAGTGGTGCAGGT 956
DB 903 GGCACAGAGTAGCAGGTGAGCGCTGTTTGGTGACATTTGGGCGCAGAGTGGTGCAGGT 962
QY 957 GAGGAGAGGTACTTTGGAGCTCCAGGTCTGCGCAGCATAGCAATGGTATTTGACAG 1016
DB 963 GAGGAGAGGTACTTTGGAGCTCCAGGTCTGCGCAGCATAGCAATGGTATTTGACAG 1022
QY 1017 GGAAGTGGGAGAGCTTTCTTGACCCAGAGAGCTGAGGGGAGCTGAACATGATTACTTG 1076
DB 1023 GGAAGTGGGAGAGCTTTCTTGACCCAGAGAGCTGAGGGGAGCTGAACATGATTACTTG 1082
QY 1077 TCTGCTTAGAGCTTTGTAAAGAGTCAAACTTAGTGTGCTCCAGGGCTTGGCCTGT 1136
DB 1083 TCTGCTTAGAGCTTTGTAAAGAGTCAAACTTAGTGTGCTCCAGGGCTTGG-CTGT 1141
QY 1137 GTGATATGAGGATAGAGGATTACTTGTGAGGCAATGTGGCATGTGGGATTTGGCAA 1196
DB 1142 GTGATATGAGGATAGAGGATTACTTGTGAGGCAATGTGGCATGTGGGATTTGGCAA 1201
QY 1197 ACTAGATTCACATCACCCACCATATATAGGCTTGCATTACACGAGGCGAGAGCACTA 1256
DB 1202 ACTAGATTCACATCACCCACCATATATAGGCTTGCATTACACGAGGCGAGAGCACTA 1261
QY 1257 GTGTGCTGCATCTTCTTACGCAAAAAA 1291
DB 1262 GTGTGCTGCATCTTCTTACGCAAAAAA 1296

RESULT 3

US-09-949-016-5115
; Sequence 5115, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5115
; LENGTH: 1558
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5115

Query Match 5.6%; Score 72.6; DB 3; Length 1558;
Best Local Similarity 59.0%; Pred. No. 1.5e-10;
Matches 148; Conservative 0; Mismatches 94; Indels 9; Gaps 1;
QY 263 ATATTATGTCATACGCGCTTGTCCCTGTGTTCTTTATCATGGGTCTCTTTGGCGTCTCAT 322
DB 803 ATATATGCTCTTCTGCTTGTGCTGGTCTTCTTCTCATGGGCTGTAGGCTTCATGAT 862
QY 323 TTGCCACCTGCTTAAGAAAGAGGCTATCGTTGTATCAACAGAGCAGACGATATATCGA 382
DB 863 CTGCCACGTGCTCAAGAAGAAGGGCTACCGCTGCCGACGCTCGAGGGGCTCTGAGCCTGA 922
QY 383 AGAGGAAAAGTTGAAAGATAGATTAATGAATGACAGTGTGAATGAAGAAACAGTGACACTGT 442
DB 923 CGATGCCAGCTTTCAGCCCTCGAGGACGATGACATG-----AATGAGGACACAGT 973
QY 443 TGGCAAAATCGTCACCTACATCATGAAATAATGAAGCGAATGCTGATGCTTTAAAGGCGAT 502
DB 974 AGAGAGATTTGTCGTGTCATCATCCAGATGAAGCCATGCTGAGGCTTTGAAGGAGAT 1033
QY 503 GGTAGCAGATA 513
DB 1034 GCTGGGGGACA 1044

RESULT 4

US-09-774-528-2
; Sequence 2, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 2

; LENGTH: 1793
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (756)..(1667)
US-09-774-528-2

Query Match 5.6%; Score 72.6; DB 3; Length 1793;
Best Local Similarity 59.0%; Pred. No. 1.7e-10;
Matches 148; Conservative 0; Mismatches 94; Indels 9; Gaps 1;
QY 263 ATATTATGTCATACGCGCTTGTCCCTGTGTTCTTTATCATGGGTCTCTTTGGCGTCTCAT 322
DB 800 ATATATGCTCTTCTGCTTGTGCTGGTCTTCTTCTCATGGGCTGTAGGCTTCATGAT 859
QY 323 TTGCCACCTGCTTAAGAAAGAGGCTATCGTTGTATCAACAGAGCAGACGATATATCGA 382
DB 860 CTGCCACGTGCTCAAGAAGAAGGGCTACCGCTGCCGACGCTCGAGGGGCTCTGAGCCTGA 919
QY 383 AGAGGAAAAGTTGAAAGATAGATTAATGAATGACAGTGTGAATGAAGAAACAGTGACACTGT 442
DB 920 CGATGCCAGCTTTCAGCCCTCGAGGACGATGACATG-----AATGAGGACACAGT 970
QY 443 TGGCAAAATCGTCACCTACATCATGAAATAATGAAGCGAATGCTGATGCTTTAAAGGCGAT 502
DB 971 AGAGAGATTTGTCGTGTCATCATCCAGATGAAGCCATGCTGAGGCTTTGAAGGAGAT 1030
QY 503 GGTAGCAGATA 513
DB 1031 GCTGGGGGACA 1041

RESULT 5

US-10-120-988-2
; Sequence 2, Application US/10120988
; Patent No. 6919193
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Feiyan
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6919193el Nucleic Acids and
; Polypeptides
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 2
; LENGTH: 1793
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (756)..(1667)
US-10-120-988-2

Query Match 5.6%; Score 72.6; DB 3; Length 1793;
Best Local Similarity 59.0%; Pred. No. 1.7e-10;
Matches 148; Conservative 0; Mismatches 94; Indels 9; Gaps 1;
QY 263 ATATTATGTCATACGCGCTTGTCCCTGTGTTCTTTATCATGGGTCTCTTTGGCGTCTCAT 322
DB 800 ATATATGCTCTTCTGCTTGTGCTGGTCTTCTTCTCATGGGCTGTAGGCTTCATGAT 859
QY 323 TTGCCACCTGCTTAAGAAAGAGGCTATCGTTGTATCAACAGAGCAGACGATATATCGA 382
DB 860 CTGCCACGTGCTCAAGAAGAAGGGCTACCGCTGCCGACGCTCGAGGGGCTCTGAGCCTGA 919


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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16044
; LENGTH: 19927
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16044

Query Match          4.0%; Score 51.4; DB 3; Length 19927;
Best Local Similarity 72.0%; Pred. No. 0.00099;
Matches 67; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 263 ATATATTGATAGCGCTTCCCTGTGTTCTTTATCATGGGTCTCTTTGGCGTCCTCAT 322
Db 532 ATATATGCTCTTCTGCTTGTGCTGTTCTTCTTCTCATGGGCTGTGTAGGCTTCATGAT 473

QY 323 TTGCCACCTGCTTAAGAAAGAAAGGCTATCGTTG 355
Db 472 CTGCCACGTGCTCAAGAAAGAGGCTACCGGTG 440

RESULT 9
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          3.5%; Score 45; DB 3; Length 4411529;
Best Local Similarity 53.0%; Pred. No. 1.5;
Matches 96; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1 CCCACGCGTCCGGCCCGCCGCTCCGGAGCGGCTCTGCCCTTCCGAGCGGGACGGGCG 60
Db 1573347 CCCAGCGCGCGCCCGCGCTGTCGATCAGCCCGCCCGCCCGCCGACCGCGGCC 1573406

QY 61 GCCCTGGGGAGAGGCGGAGCGACCGCGGATGGCTCCCGCGGCACTCCCGGGTCCG 120
Db 1573407 TGACCGGTGGCGCGGACCGCGCTTCCCGCGTTCGCTACAGGATCCCGCGGCCCG 1573466

QY 121 CCTCTCTAGCCGCTGCTGTTCTTGTGGAGGCGCGGTGAGTTCCCGCTGCTGCTCCG 180
Db 1573467 CCGGCTTGCCTGGTCTCCCGCGGCCCGCTGCGGCGCGGTGCGGATCAGCGGGCGCCCGAGC 1573526

QY 181 A 181
Db 1573527 A 1573527

RESULT 10
US-09-621-976-10505
; Sequence 10505, Application US/09621976
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; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 10505
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-621-976-10505

Query Match          3.5%; Score 44.6; DB 3; Length 433;
Best Local Similarity 55.6%; Pred. No. 0.011;
Matches 75; Conservative 5; Mismatches 55; Indels 0; Gaps 0;

QY 78 CGAAGCGACCGCGCGATGGCTCCGCGGCACTCCCGGGTCCCGCTCTAGCGGTGCT 137
Db 226 CGAAGAGGCTGTGCGAGCCCTDCCCGGSCCTCCCGAGGGCCCGCCCTCTCTCTGCC 285

QY 138 GTCTTGTGGAGGCGCGCTGAGTTGCCCGCTGGTGGCTCCGACATGGAGCAGCGCG 197
Db 286 TGCTGCGTGGAGGCGAGCCATGGGAAGGAGCTGGGCTGGGGAGCGANMSCC 345

QY 198 ACATTGCATCCAGA 212
Db 346 ATGTTGWTTCCTGA 360

RESULT 11
US-09-902-540-8667
; Sequence 8667, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8667
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-8667

Query Match          3.4%; Score 44.4; DB 3; Length 573;
Best Local Similarity 49.6%; Pred. No. 0.015;
Matches 114; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 4 ACCGCTCCGCGCCCGCGGCTCCGAGCGGCTCTGCCCTTCCCGAGCGCGGACGCGCGCC 63
Db 164 ACCCTTCCCGAAGGCGGCCAGGCCCTGCTCCCGAAGTCGAGCGGCTGTGGCGAGG 223

QY 64 CTGGGGAGAGGCGGAGCGAGCGCGCGATGGCTCCCGCGGCACTCCCGGGTCCCGCG 123
Db 224 CGCTGGCGCGCGCGGATGTCTCGCGGTGGCCCCCGCTGGAGAGCTGTGTGGCGCGC 283

QY 124 TCCTAGCGCTGCTGTCTTCTGTTGGAGGCGCGGTGAGTTCCCGCTGCTGCTCCGACA 183
Db 284 TGCTGGCCACACGCGGCGGCTCTGCCACACCGCGCGGACGCTGTGGAGCGCGGAGA 343

QY 184 ATGGAGGACCGCCGACATTGCACTCCAGAACAGAGACGACCCCGTCCGCC 233
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Db 344 CGGCTGGCGCGCGGCGGAGGCTGGAGCGCGCGCGCACCCGACGCGC 393

RESULT 12

US-09-902-540-918
; Sequence 918, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wisigand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 918
; LENGTH: 9191
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-918

Query Match 3.4%; Score 44.4; DB 3; Length 9191;
Best Local Similarity 49.6%; Pred. No. 0.069;
Matches 114; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
Qy 4 ACGGTCTCGGCGCGCGCTCCGAGCGGCTCTGCTTCCGAGCGCGGAGCGCGCGCC 63
Db 2956 ACCCTTCCGCAAGCGCGCCAGGCGCTCTCCCGAAGTCGAGCGGCTGTCGGCGAGG 3015
Qy 64 CTGGGGAGGAGGCGAAGCAGCGGCGATGGCTCCGCGGCGACTCCCGGGTCCGCG 123
Db 3016 CGCTGGCGCGCGCGGAGATCTCGGCGGTGGCGCCCTCGAGAGCTGTGGCGCGC 3075
Qy 124 TCCTAGCGCTGTCTTCTCGTGGAGCGCGCTGAGTTCCCGCTGGTCTCCGAGCA 183
Db 3076 TGCTGGCCACGCGGAGCGCTCTGCCACACCGCGCGGAGCTTGAGGCGCGGAGA 3135
Qy 184 ATGGAGAGCGCGCACATTCACCTCCAGACAGAGACGACCCGTCGCGCC 233
Db 3136 CGGCTTGGCGCGCGCGAGGAGTGGAGCGCGCGCGCGCACCCGACGCGC 3185

RESULT 13

US-10-012-231A-259
; Sequence 259, Application US/10012231A
; Patent No. 6924355
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C23
; CURRENT APPLICATION NUMBER: US/10/012,231A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 259
; LENGTH: 4563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3635
; OTHER INFORMATION: unknown base
US-10-012-231A-259

Query Match 3.3%; Score 43; DB 3; Length 4563;
Best Local Similarity 53.2%; Pred. No. 0.12;
Matches 91; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
Qy 2 CCACGCGTCCCGCGCGCGCTCCGAGCGGCTCTGCTTCCGAGCGCGGAGCGCGCG 61
Db 398 CCGTGGCGGGGCGAGCGGCTGAGGGCGCGCGGCGCTGCGCGCGCGCGCGCGCG 457
Qy 62 CCCTGGGGAGGAGGCGAGCGAGCGGCGCATGGCTCCGCGGGCACTCCCGGGTCCGC 121
Db 458 GCGCGCGCGCGCGCGGCGAGCGCGCGGCGCATGGCGCGCGCGCGCGCGCGCTGGCT 517
Qy 122 CGTCTAGCGCGCTCTGCTTCTGTTGGAGGCGCGGTGAGTTCCGCGCTGCT 172
Db 518 CAGCGTGTGCTCGGGCTGCTCTGGGCTTCTGCTGCGCTCGCGGCTCGT 568

RESULT 14

US-10-015-389A-259
; Sequence 259, Application US/10015389A
; Patent No. 6936436
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C48
; CURRENT APPLICATION NUMBER: US/10/015,389A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 259
; LENGTH: 4563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3635
; OTHER INFORMATION: unknown base
US-10-015-389A-259

Query Match 3.3%; Score 43; DB 3; Length 4563;
Best Local Similarity 53.2%; Pred. No. 0.12;
Matches 91; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
Qy 2 CCACGCGTCCCGCGCGCGCTCCGAGCGGCTCTGCTTCCGAGCGCGGAGCGCGCG 61
Db 398 CCGTGGCGGGGCGAGCGGCTGAGGGCGCGCGGAGCTTGGCGCGCGCGCGCGCG 457
Qy 62 CCCTGGGGAGGAGGCGAGCGAGCGGCGCATGGCTCCGCGGGCACTCCCGGGTCCGC 121

Db 458 GCGCGCGCCGCGCGCGGAGCGCGCGGCGCATGCGCGCGCGCGCGCGCGCTGGCT 517
Qy 122 CGTCCTAGCCGCTGCTCTTCGTGGGAGGCGCGCTGAGTTCCGCGCTGGT 172
Db 518 CAGCGTCTGCTCGCGGCTCGTCTGGGCTTCGTGCTGCGCTCGCGGCTCGT 568

RESULT 15

US-10-006-768A-259
; Sequence 259, Application US/10006768A
; Patent No. 6936697
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC10
; CURRENT APPLICATION NUMBER: US/10/006.768A
; CURRENT FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 259
; LENGTH: 4563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3635
; OTHER INFORMATION: unknown base
US-10-006-768A-259

Query Match 3.3%; Score 43; DB 3; Length 4563;
Best Local Similarity 53.2%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 91; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
Qy 2 CCACGCTCCGCGCCGCGGCTCCGAGCGGCTCTGCTTCCGAGCGCGGACGCGCG 61
Db 398 CCGTGGCGGGGCGAGCGGCTGAGGGCGCGCGGAGCTGCGGCGCGCGCGCGCG 457
Qy 62 CCCTGGGGAGAGGCGAGCGACGCGGCGATGGCTCCCGGGGCACTCCCGGGTCCGC 121
Db 458 GCGCGCGCCGCGCGGCGGAGCGCGCGGCGCATGCGCGCGCGCGCGCGCGCTGGCT 517
Qy 122 CGTCCTAGCCGCTGCTCTTCGTGGGAGGCGCGCTGAGTTCCGCGCTGGT 172
Db 518 CAGCGTCTGCTCGGGCTCGTCTGGGCTTCGTGCTGCGCTCGCGGCTCGT 568

Search completed: February 23, 2006, 15:12:58
Job time : 274 secs